

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requestor's Name: David Lukton Examiner number: 71263 Date: 5/24/04

Art Unit: 1653 Phone number: 571-272-0952 Serial Number:
09-765105

Mail Box: 3-C-70 Examiner Rm: 3-B-75 Results format: paper

Title of Invention: C-TERMINAL MODIFIED OXAMYL
DIPEPTIDES AS INHIBITORS OF THE ICE-CED-3 FAMILY OF
CYSTEINE PROTEASES

Applicants: KARANEWSKY, DONALD S., TERNANSKY, ROBERT
J., LINTON, STEVEN D., DINH, THANG

Earliest Priority Date: 7/2/98

* * * *

Please search the sequences in this case

182 AA's

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: _____	NA Sequence (#) _____	STN _____
Searcher Phone #: _____	AA Sequence (#) <u>2</u>	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>5/24/04</u>	Bibliographic _____	Dr. Link _____
Date Completed: <u>5/25/04</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems <u>QSP</u>
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Fee: _____	Other _____	Other (specify) _____

Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions **.nrpm** and **.nrpn**

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions **.rapm** and **.rapn**

Because they contain data that is confidential, the results of Pending database searches should not be left in the case .



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 122770

TO: David Lukton
Location: rem/3b75/3c70
Art Unit: 1653
Tuesday, May 25, 2004

Case Serial Number: 09/765105

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Lukton,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart



STIC SEARCH RESULT FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or *contact*:

Mary Hale, Information Branch Supervisor
571-272-2507 Remsen E01 D86

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library Remsen Bldg.



GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 24, 2004, 14:36:17 / Search time 51 seconds
(without alignments)
22.161 Million cell updates/sec

Title: US-09-765-105A-1

Perfect score: 21

Sequence: 1 YVAD 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Jan04.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	21	100.0	4	2	AAR34789 Interleuk
2	21	100.0	4	2	AAR34621 Chromoph
3	21	100.0	4	2	AAR32544 Chromoph
4	21	100.0	4	2	AAR34822 Chromoph
5	21	100.0	4	2	AAR51047 Sequence
6	21	100.0	4	2	AAR77200 Cell prol
7	21	100.0	4	2	AAR95702 Tetrapept
8	21	100.0	4	2	AAR98753 Asp-ase i
9	21	100.0	4	2	AAR00214 Ich-2 sub
10	21	100.0	4	2	AAR06453 ICE pepti
11	21	100.0	4	2	AAR45979 Cysteine
12	21	100.0	4	2	AAR76199 Mouse cas
13	21	100.0	4	2	AAR52749 Aminometh
14	21	100.0	4	2	ABP71236 ICE-speci
15	21	100.0	4	2	AAR56304 Peptide c
16	21	100.0	4	2	AAR65067 ICE bindi
17	21	100.0	4	2	AAR15619 Peptide u
18	21	100.0	4	2	AAR30071 N-substit
19	21	100.0	4	2	AAR04112 Enzyme co
20	21	100.0	4	2	AAR68555 Interleuk
21	21	100.0	4	2	AAR24410 Caspase p
22	21	100.0	4	2	AAR99674 ICE prote
23	21	100.0	4	2	AAR94092 Protease
24	21	100.0	4	2	AAR94094 Protease
25	21	100.0	4	3	AAR69647 Caspase i

26	21	100.0	4	3	AAV99959	Tetrapept
27	21	100.0	4	3	AAV49941	Synthetic
28	21	100.0	4	3	AAB26850	Synthetic
29	21	100.0	4	3	AAV80783	Fluoropho
30	21	100.0	4	3	AAV69867	ICE cleav
31	21	100.0	4	3	AAV67492	Caspase 1
32	21	100.0	4	3	AAV81938	APP agon
33	21	100.0	4	3	AAV87640	Caspase s
34	21	100.0	4	3	AAV826703	Caspase s
35	21	100.0	4	3	AAB03094	Substrate
36	21	100.0	4	3	AAV56893	Caspase i
37	21	100.0	4	3	AAV57442	Peptide A
38	21	100.0	4	3	AAB28539	Caspase-1
39	21	100.0	4	3	AAB32119	Tetrapept
40	21	100.0	4	4	AAB59584	Caspase-1
41	21	100.0	4	4	AAG62548	Cresyl vi
42	21	100.0	4	4	AAG67379	Peptide s
43	21	100.0	4	4	AAV72472	VVAD pept
44	21	100.0	4	4	AAG64408	Caspase p
45	21	100.0	4	4	AAB91890	Apoptosis

ALIGNMENTS

RESULT 1
AAR34789
ID AAR34789 standard; peptide; 4 AA.
XX AAR34789;
AC
XX
XX 25-MAR-2003 (revised)
DT 08-JUL-1993 (first entry)
XX
DE Interleukin-1beta convertase activity determining peptide.
XX ICE; interleukin-1beta convertase; activity; chromophore contg;
KW monitoring; IL-1 mediated diseases; ICE inhibitor evaluation; diagnosis.
XX Synthetic.
XX Key Location/Qualifiers
FH Modified-site 1 /note= "N-acetyl-Tyr"
FT Modified-site 4
FT Modified-site 4 /note= "Asp-p-nitroanilide, Asp-6-aminoquinoline amide or
FT FT Asp-7-amino-4-methylcoumarin amide"
XX EF533226-A2.
XX 24-MAR-1993.
XX 08-AUG-1992; 92EP-00202449.
XX 16-AUG-1991; 91US-00746524.
XX 17-DEC-1991; 91US-00808996.
XX (MERI) MERCK & CO INC.
XX Chapman KT, Maccoss M, Mumford RA, Thornberry NA, Weidner JR;
XX WPI; 1993-095531/12.
XX New chromophore-contg. peptide derivs. - for determining interleukin-1-
XX beta convertase activity in the diagnosis of inflammatory and immune-
XX based conditions.
XX Example; Page 26; 41pp; English.
XX The peptide is a chromophore contg. compound which is useful in
XX determining interleukin-1beta convertase (ICE) activity and is therefore
XX useful in diagnosis and monitoring of IL-1 mediated diseases or in
XX evaluation of ICE inhibitors. IL-1 has been implicated in meningitis,

CC salpingitis, complications of septic shock, disseminated intravascular
CC coagulation; adult respiratory distress syndrome, inflammation due to
CC antigen, antibody, and/or complement deposition, arthritis, cholangitis,
CC colitis, encephalitis, endocarditis, glomerulonephritis, hepatitis,
CC myocarditis, pancreatitis, pericarditis, reperfusion injury, and
CC - rejection. Immune based diseases include hypersensitivity, graft
CC diabetes mellitus and multiple sclerosis. IL-1 has also been implicated
CC in treatment of bone and cartilage resorption, or diseases causing
CC excessive extracellular matrix deposition. These include periodontal
CC disease, interstitial pulmonary fibrosis, cirrhosis, systemic sclerosis,
CC or keloid formation. To use the peptide in an assay, the peptide, ICE, or
CC cleaves the chromophore bond, and the ICE activity is then determined by
CC spectrophotometric or fluorimetric analysis. Leucine amino- peptidase
CC microsomal (LAPM) is the most pref. enzyme in the disclosure. The peptide
CC is used in concns. of 1 uM to 10 mM. (Updated on 25-MAR-2003 to correct
CC PN field.)
XX Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
Db 1 YVAD 4

RESULT 2
ID AAR34621 standard; peptide; 4 AA.
XX AAR34621;
XX AAR34621;
DT 25-MAR-2003 (revised)
DT 12-NOV-1992 (first entry)
XX Chromophore-contg. cpd. for determining ICE activity (1).
XX Interleukin-lbета; IL-lb; inflammation; immune; disease; diagnosis;
KW p-nitroanilide.
XX Synthetic.
XX Key Location/Qualifiers
FT Modified-site 1 /note= "N-acetyl-tyrosinyl"
FT Modified-site 4 /note= "aspartic acid p-nitroanilide"

EP528487-A2.
24-FEB-1993.
08-AUG-1992; 92EP-00202450.
16-AUG-1991; 91US-00746455.
17-DEC-1991; 91US-00808994.
(MERI) MERCK & CO INC.
Chapman KT, Thornberry NA, Maccoss M, Weidner JR, Mumford RA;
Hagmann WK;
WPI; 1993-060350/08.
New chromophore-contg. cpds. - for determining interleukin-lbета
PT convertase activity in diagnosis of inflammatory or immune-based
PT disorders.
XX Claim 9; Page 42; 42pp; English.

XX The cpd. is used for determining interleukin-lbета convertase (ICE)
CC activity. ICE has been implicated in inflammatory and immune-based
CC diseases including diseases of the lungs and airways, CNS, eyes, ears,
CC joints, bones and connective tissues, cardiovascular system (including
CC the pericardium), GI and urogenital systems and skin and mucosal
CC membranes. (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
Db 1 YVAD 4

RESULT 3
ID AAR32544 standard; peptide; 4 AA.
XX AAR32544;
XX AAR32544;
DT 25-MAR-2003 (revised)
DT 12-NOV-1992 (first entry)
XX Chromophore-contg. cpd. for determining ICE activity (5).
XX Interleukin-lbета; IL-lb; inflammation; immune; disease; diagnosis;
KW 7-amino-4-methylcoumarin.
XX Synthetic.
XX Key Location/Qualifiers
FT Modified-site 1 /note= "N-acetyl-tyrosinyl"
FT Modified-site 4 /note= "aspartic acid 7-amino-4-methylcoumarin"

EP528487-A2.
24-FEB-1993.
08-AUG-1992; 92EP-00202450.
16-AUG-1991; 91US-00746455.
17-DEC-1991; 91US-00808994.
(MERI) MERCK & CO INC.
Chapman KT, Thornberry NA, Maccoss M, Weidner JR, Mumford RA;
Hagmann WK;
WPI; 1993-060350/08.
New chromophore-contg. cpds. - for determining interleukin-lbета
PT convertase activity in diagnosis of inflammatory or immune-based
PT disorders.
XX Example 8; Page 31; 42pp; English.
XX The cpd. is used for determining interleukin-lbета convertase (ICE)
CC activity. ICE has been implicated in inflammatory and immune-based
CC diseases including diseases of the lungs and airways, CNS, eyes, ears,
CC joints, bones and connective tissues, cardiovascular system (including
CC the pericardium), GI and urogenital systems and skin and mucosal
CC membranes. (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
DB 1 YVAD 4

RESULT 4
AAR34622
ID AAR34622 standard; peptide; 4 AA.
XX
AC AAR34622;
XX
XX
DT 25-MAR-2003 (revised)
DT 12-NOV-1992 (first entry)
XX
XX Chromophore-contg. cpd. for determining ICE activity (2).
XX
KW Interleukin-1b; IL-1b; inflammation; immune; disease; diagnosis;
KW 6-aminoguanoline amide.
XX
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT Modified-site 4 /note= "N-acetyl-tyrosinyl"
FT Modified-site 4
FT Modified-site 4 /note= "aspartic acid 6-aminoguanoline amide"
XX
XX EP528487-A2.
XX
XX 24-FEB-1993.
XX
XX 08-AUG-1992; 92EP-00202450.
XX
XX 16-AUG-1991; 91US-00746455.
XX 17-DEC-1991; 91US-00808994.
XX
XX (MERI) MERCK & CO INC.
XX
XX Chapman KT, Thornberry NA, Maccoss M, Weidner JR, Mumford RA;
XX Hagmann WK;
XX
XX WPI; 1993-060350/08.
XX
XX New chromophore-contg. cpds. - for determining interleukin-1b
FT convertase activity in diagnosis of inflammatory or immune-based
PT disorders.
XX
XX Claim 9; Page 42; 42pp; English.
XX
XX The cpd. is used for determining interleukin-1b convertase (ICE)
CC activity. ICE has been implicated in inflammatory and immune-based
CC diseases including diseases of the lungs and airways, CNS, eyes, ears,
CC joints, bones and connective tissues, cardiovascular system (including
CC the pericardium), GI and urogenital systems and skin and mucosal
CC membranes. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 4 AA;
QY 1 YVAD 4
DB 1 YVAD 4

Query Match 100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
DB 1 YVAD 4

RESULT 5
AAR51047
ID AAR51047 standard; protein; 4 AA.

XX AAR51047;
AC
XX
DT 25-MAR-2003 (revised)
DT 07-OCT-1994 (first entry)
XX
XX Sequence of tetrapeptide aldehyde inhibitor of murine precursor
DE interleukin-1 beta (pre-IL-1 beta) converting enzyme (ICE).
XX
XX Interleukin-1 beta converting enzyme; mature interleukin; inhibitor; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT Modified-site 4 /label= Ac
FT Modified-site 4 /label= CHO
XX
XX WO9406906-A1.
XX
XX 31-MAR-1994.
XX
XX 09-SEP-1993; 93WO-US008479.
XX
XX 18-SEP-1992; 92US-00947330.
XX
XX (MERI) MERCK & CO INC.
XX
XX Molineaux SM, Rolando AM, Casano FJ;
XX WPI; 1994-118456/14.
XX
XX DNA encoding murine precursor interleukin 1 beta converting enzyme - for
FT producing ICE and its subunits and for identification of inhibitors of
PT ICE activity.
XX
XX Disclosure; Page 15; 87pp; English.
XX
XX cDNA encoding murine pre-IL-1 beta converting enzyme (ICE) was isolated
CC from IL-1 producing mouse cells. Murine ICE cleaves the peptide bond
CC between Asp17 and Val118 of murine precursor IL-1 beta, and the peptide
CC bond between Asp27 and Gly28. The preferred cells for isolating murine
CC ICE-encoding DNA include mouse macrophages and (pref.) WEHI-3 cells.
CC Tetrapeptide aldehyde inhibitor Ac-YVAD-CHO inhibits murine ICE with a Ki
CC of 3nM or less. This is comparable to the potency observed against the
CC human enzyme and suggests that the active sites of both convertases are
CC similar. Ac-YVAD-CHO was used to make an affinity ligand (Ac-YVAD-CHO)
CC with which to purify active ICE. Due to the enzyme's unusual substrate
CC specificity, an affinity column can be used to purify ICE in a single
CC step from a crude cellular lysate. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
XX Sequence 4 AA;
QY 1 YVAD 4
DB 1 YVAD 4

Query Match 100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
DB 1 YVAD 4

RESULT 6
AAR77200
ID AAR77200 standard; peptide; 4 AA.
XX
XX AAR77200;
AC
XX
XX 27-FEB-1996 (first entry)
DT
XX
XX Cell proliferation enzyme proteinase activity substrate peptide #5.
DE

XX Proteinase; cell growth-stimulating protein; hydrolysis;
KW macrophage chemotactic action; serine protease inhibitor; wound;
KW gastric ulcer; leg ulcer; bed sore.
XX
XX Synthetic.
XX
XX
XX Key Location/Qualifiers
FH Modified-site 1
FT /label= Acyl-Tyr
FT Modified-site 4
FT /note= "Modified by 4-methyl-coumaryl-7-amide"
XX
XX
XX EP661293-A2.
XX
XX 05-JUL-1995.
XX
XX 22-DEC-1994; 94EP-00120406.
XX
XX 29-DEC-1993; 93JP-00351225.
XX
XX (SANW) SANWA KAGAKU KENKYUSHO CO.
XX
XX Yamaguchi T, Uesaka H, Watanabe K, Awaysa J;
XX WPI; 1995-233274/31.
XX
XX Protein derived from Clostridium perfringens FERM BP-4584 - stimulates
PT cell proliferation and has macrophage chemotactic action.
XX
XX Example; Page 8; 14pp; English.
XX
XX The sequences given in AAR77196-200 are peptides which were used to
CC demonstrate the proteinase activity of the cell growth-stimulating
CC protein of the invention. The protein was seen to selectively hydrolyse
CC synthetic substrates having an aromatic amino acid at the C-terminal. The
CC response to the peptide given in AAR77196 was particularly high. The cell
CC growth-stimulating protein has a mol. wt. of 420 +/- 40 kD and a single
CC subunit mol. wt. of 130 +/- 20 kD. It has an isoelectric point of 4.8
CC and has cell growth stimulating action and macrophage chemotactic
CC action, as well as proteinase activity. Its enzymatic activity decreases
CC in the presence of a serine protease inhibitor, increase in the presence
CC of various metal ions, and is stabilised in the presence of calcium ion.
CC The protein is particularly useful for the treatment of wounds, gastric
CC and leg ulcers, eg. bed sores
XX
XX Sequence 4 AA;
SQ
Query Match 100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YVAD 4
DB 1 YVAD 4
RESULT 7
AAR95702
ID AAR95702 standard; peptide; 4 AA.
XX
XX AAR95702;
AC
XX 01-AUG-1996 (first entry)
DT
XX Tetrapeptide aldehyde inhibitor 'Ala'.
XX
XX Interleukin-1-beta converting enzyme; ICE; inhibitor; inflammation;
KW apoptosis; protein engineering; crystal structure.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH

FT Modified-site 1
PT /note= "N-terminal acetyl gp."
XX
XX WO9535367-A1.
PN
XX
XX 28-DEC-1995.
PD
XX
XX 16-JUN-1995; 95WO-US007619.
PF
XX
XX 17-JUN-1994; 94US-00261582.
PR
XX
XX (VERT-) VERTEX PHARM INC.
PA
XX
XX Wilson KP, Griffith JP, Kim EE, Livingston DJ;
PI
XX
XX WPI; 1996-058405/06.
DR
XX
XX Interleukin-1 beta converting enzyme (ICE) crystal structure - useful for
PT designing and evaluating opds., esp. inhibitors that bind to ICE active
PT site or accessory binding site.
XX
XX Example 1; Page 33; 104pp; English.
PS
XX
XX A tetrapeptide aldehyde (AAR95702) used in 2x molar excess completely
CC inhibited the activity of autoprocesed interleukin-1 beta converting
CC enzyme (ICE) (see also AAR95701) obtcd. By expression of human ICE cDNA in
CC Escherichia coli. The protein-inhibitor complex was purified, and
CC crystals of ICE in complex with the inhibitor were grown by vapour
CC diffusion. These were used to determine the crystal structure of ICE,
CC useful e.g. in the design of novel ICE inhibitors
XX
XX Sequence 4 AA;
SQ
Query Match 100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YVAD 4
DB 1 YVAD 4
RESULT 8
AAR98753
ID AAR98753 standard; peptide; 4 AA.
XX
XX AAR98753;
AC
XX
XX 17-DEC-1996 (first entry)
DT
XX
XX Asp-ase inhibitor B.
DE
XX
XX Interleukin-1 beta converting enzyme; ICE; Ced-3; Asp-ase inhibitor;
KW cell death; apoptosis; neural degeneration.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH
FT Misc-difference 1
FT /note= "N-terminal acylation"
FT Misc-difference 4
FT /note= "C-terminal aldehyde gp."
XX
XX WO9625946-A1.
PN
XX
XX 29-AUG-1996.
PD
XX
XX 23-FEB-1996; 96WO-US002473.
PF
XX
XX 24-FEB-1995; 95US-00394189.
PR
XX
XX (VASI) MASSACHUSETTS INST TECHNOLOGY.
PA
XX

MATCHES	4,	CONSERVATIVE	V,	HIGHSCORES	V,	ANALYSIS	V,	CASES
Oy	1	YVAD	4					

FT Modified-site 4
 FT /note= "the C-terminal is condensed onto 7-amino- 4-
 FT methyl-coumarin via an amide linkage"
 XX
 FN GB2324529-A.
 XX
 XX 28-OCT-1998.
 XX
 XX 20-FEB-1998; 98GB-00003559.
 XX
 XX 21-FEB-1997; 97US-0039656P.
 XX
 XX (MERI) MERCK & CO INC.
 XX
 XX Chapman KT, Nicholson D, Rano T, Thornberry N;
 XX WPI; 1998-523841/45.
 XX
 XX New tetrapeptide coumarin derivatives - useful in combinatorial libraries
 PT to identify substrate specificity of cysteine or serine proteases e.g.
 PT interleukin-1 converting enzyme.
 XX
 XX Claim 3; Page 40; 49pp; English.
 XX
 XX The peptide is a specifically claimed example of new aminomethyl-
 CC coumarin-labelled tetrapeptides of formula Ac-Xaa-Xaa-Asp-AMC. The
 CC tetrapeptides are used to generate a fluorescent positional scanning
 CC synthetic combinatorial library for the investigation of the substrate
 CC specificity of cysteine and serine proteases, e.g. in the analysis of
 CC interleukin-1 beta converting enzyme substrate and other caspase
 CC substrates, and to identify inhibitors which may mediate inflammations.
 CC The library preferably comprises a mixture of at least 200 of the
 CC tetrapeptides
 XX
 XX Sequence 4 AA;
 SQ
 Query Match 100.0%; Score 21; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PR 11-OCT-1996; 96US-0028313P.
 XX (WARN) WARNER LAMBERT CO.
 XX
 XX Albrecht HP, Allen HJ, Brady KD, Harter WG, Kostlan CR, Roth BD;
 PI Walker N;
 XX
 XX WPI; 1998-312002/27.
 XX
 XX New sulphonamide compounds - are inhibitors of interleukin-1beta
 PT converting enzyme and caspase-4, used for treating stroke and
 PT inflammatory diseases, etc.
 XX
 XX Example 6; Page 35; 56pp; English.
 XX
 XX The invention provides sulphonamide compounds of specified formula and
 CC their salts, esters, amides and prodrugs. The sulphonamide compounds are
 CC used for inhibiting interleukin 1beta converting enzyme (ICE), inhibiting
 CC caspase-4, treating or preventing stroke, inflammatory diseases e.g.
 CC arthritis, inflammatory bowel disease, septic shock, reperfusion injury,
 CC Alzheimer's disease and shigellosis. The present sequence represents a
 CC peptide substrate specific for ICE
 XX
 XX Sequence 4 AA;
 SQ
 Query Match 100.0%; Score 21; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
 DB 1 YVAD 4
 RESULT 14
 ABP71236
 ID ABP71236 standard; peptide; 4 AA.
 XX
 XX AC ABP71236;
 XX
 XX 28-APR-2003 (first entry)
 XX
 XX ICE-specific peptide substrate.
 DE
 XX Ich-2; ICE; sulphonamide; interleukin 1beta converting enzyme; caspase-4;
 KW stroke; inflammatory disease; septic shock; reperfusion injury;
 KW Alzheimer's disease; shigellosis.
 XX
 XX Synthetic.
 OS
 XX
 XX Key Location/Qualifiers
 FH Modified-site 1
 FT /note= "N-terminal acetylation"
 FT Modified-site 4
 FT /note= "C-terminal Asp-pNA"
 FT
 XX WO9816505-A1.
 XX
 XX 23-APR-1998.
 XX
 XX 09-OCT-1997; 97WO-US018396.
 XX

QY 1 YVAD 4
 DB 1 YVAD 4
 RESULT 15
 AAWS6304
 ID AAWS6304 standard; peptide; 4 AA.
 XX
 XX AC AAWS6304;
 XX
 XX 22-JUL-1998 (first entry)
 DT
 XX
 XX Peptide cleaved by interleukin-1-beta-converting enzyme-like protein.
 DE
 XX N-acetyl-YVAD-methyl coumarinamide; MCA;
 KW interleukin-1- beta converting enzyme-like activity; ICE activity;
 KW cysteine protease; investigation; substrate specificity.
 XX
 XX Synthetic.
 OS
 XX
 XX JP1009075-A.
 XX
 XX 21-APR-1998.
 PD
 XX 30-SEP-1996; 96JP-00276813.
 XX
 XX 30-SEP-1996; 96JP-00276813.
 XX
 XX (SHIS) SHISEIDO CO LTD.
 PA
 XX
 XX WPI; 1998-289868/26.
 DR
 XX Protein with interleukin-1-beta converting enzyme-like activity - useful
 PT in investigation of substrate specificity in, e.g. Parkinson's disease.
 FT
 XX Disclosure; Page 2; 5pp; Japanese.
 PS
 XX The present sequence, N-acetyl-YVAD-methyl coumarinamide (MCA),
 CC represents a sequence that is cleaved by a protein with interleukin-1-
 CC beta converting enzyme (ICE)-like activity. The protein, which is
 CC obtained from human keratinocytes, has a relative molecular weight of 80
 CC kDa. The ICE protein is part of the cysteine protease family and is
 CC useful for investigation of the mechanism of substrate specificity (e.g.

CC Alzheimer's disease, Parkinson's disease, autoimmune disease, lymphoma,
CC cancer and apoptosis)
XX
SQ Sequence 4 AA;
Query Match 100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. NO. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YVAD 4
Db 1 YVAD 4

Search completed: May 24, 2004, 14:38:15
Job time : 53 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 24, 2004, 14:36:17 ; Search time 16.5 Seconds
(without alignments)
12.515 Million cell updates/sec

Title: US-09-765-105A-1

Perfect score: 21

Sequence: 1 YVAD 4

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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6: /cgn2_6/ptodata/2/iaa/backfiles.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	21	100.0	4	1 US-08-446-925-10	Sequence 10, Appli
3	21	100.0	4	1 US-08-464-964-1	Sequence 1, Appli
4	21	100.0	4	1 US-08-464-964-2	Sequence 2, Appli
5	21	100.0	4	1 US-08-700-716-1	Sequence 1, Appli
6	21	100.0	4	1 US-08-700-716-16	Sequence 16, Appli
7	21	100.0	4	1 US-08-592-029-4	Sequence 4, Appli
8	21	100.0	4	1 US-08-592-029-5	Sequence 5, Appli
9	21	100.0	4	1 US-08-777-208-8	Sequence 8, Appli
10	21	100.0	4	2 US-08-800-007A-11	Sequence 11, Appli
11	21	100.0	4	2 US-08-440-898-1	Sequence 1, Appli
12	21	100.0	4	2 US-08-440-898-2	Sequence 2, Appli
13	21	100.0	4	2 US-09-067-053-1	Sequence 1, Appli
14	21	100.0	4	2 US-09-067-053-16	Sequence 16, Appli
15	21	100.0	4	2 US-09-146-331-10	Sequence 10, Appli
16	21	100.0	4	2 US-08-394-189B-16	Sequence 16, Appli
17	21	100.0	4	2 US-08-394-189B-17	Sequence 17, Appli
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19	21	100.0	4	2 US-08-828-941A-2	Sequence 2, Appli
20	21	100.0	4	2 US-08-883-632-4	Sequence 4, Appli
21	21	100.0	4	2 US-08-883-632-5	Sequence 5, Appli
22	21	100.0	4	2 US-08-915-414A-2	Sequence 2, Appli
23	21	100.0	4	2 US-08-592-013A-4	Sequence 4, Appli
24	21	100.0	4	2 US-08-592-013A-5	Sequence 5, Appli
25	21	100.0	4	2 US-08-896-885-10	Sequence 10, Appli
26	21	100.0	4	2 US-08-712-878-1	Sequence 1, Appli
27	21	100.0	4	2 US-08-712-878-8	Sequence 8, Appli

28	21	100.0	4	2 US-08-712-878-9	Sequence 9, Appli
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30	21	100.0	4	3 US-08-465-216-2	Sequence 2, Appli
31	21	100.0	4	3 US-09-017-276-1	Sequence 1, Appli
32	21	100.0	4	3 US-08-761-483-1	Sequence 1, Appli
33	21	100.0	4	3 US-08-761-483-2	Sequence 2, Appli
34	21	100.0	4	3 US-08-761-483-5	Sequence 5, Appli
35	21	100.0	4	3 US-08-761-483-6	Sequence 6, Appli
36	21	100.0	4	3 US-08-761-483-11	Sequence 11, Appli
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38	21	100.0	4	3 US-09-130-193-3	Sequence 3, Appli
39	21	100.0	4	3 US-09-357-953-2	Sequence 2, Appli
40	21	100.0	4	3 US-09-309-003-2	Sequence 2, Appli
41	21	100.0	4	3 US/08/869	Sequence 2, Appli
42	21	100.0	4	3 US-09-257-218-83	Sequence 83, Appli
43	21	100.0	4	3 US-09-311-760-83	Sequence 83, Appli
44	21	100.0	4	3 US-09-291-692-72	Sequence 72, Appli
45	21	100.0	4	3 US-08-665-643A-44	Sequence 44, Appli

ALIGNMENTS

RESULT 1
US-08-354-685-1
; Sequence 1, Application US/08354685
; Patent No. 5496695
; GENERAL INFORMATION:
; APPLICANT: Daumy, Gaston C.
; APPLICANT: Reiter, Lawrence A.
; TITLE OF INVENTION: PARA-NITROANILIDE PEPTIDES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Peter C. Richardson
; STREET: 235 East 42nd Street, 20th Floor
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10017-5755
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/354,685
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 981,153
; FILING DATE: 24-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Strassburger, Philip C.
; REGISTRATION NUMBER: 34,258
; REFERENCE/DOCKET NUMBER: PC8352
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)573-5731
; TELEFAX: (212)573-1939
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; US-08-354-685-1

Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YVAD 4


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; APPLICANT: Livingston, David J
; TITLE OF INVENTION: INHIBITORS OF INTERLEUKIN-1 BETA
; TITLE OF INVENTION: CONVERTING ENZYME
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr.
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,964
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/440,898
; FILING DATE: 25-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/405,581
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/261,452
; FILING DATE: 17-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr, James F
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: VPI/94-04 CIPRI DIVI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
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; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /product= "OTHER"
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; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "aspartic acid is derivatized with
; OTHER INFORMATION: amino-4-methylcoumarin"
; US-08-464-964-2
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; Query Match 100.0%; Score 21; DB 1; Length 4;
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; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 1 YVAD 4
; Db 1 YVAD 4
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; RESULT 5
; US-08-700-716-1
; Sequence 1, Application US/08700716
; Patent No. 5744451
; GENERAL INFORMATION:
; APPLICANT: Allen, Hamish J
; APPLICANT: Banerjee, Subhashis
; APPLICANT: Brady, Kenneth D
; APPLICANT: Hodges, John C
; APPLICANT: Kostlan, Catherine R
; APPLICANT: Talanian, Robert V
; TITLE OF INVENTION: N-Substituted Glutamic Acid Derivatives
; TITLE OF INVENTION: with Interleukin-1 Converting Enzyme Inhibitory Activity
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Elizabeth M. Anderson
; STREET: 2800 Plymouth Road
; CITY: Ann Arbor
; STATE: MI
; COUNTRY: US
; ZIP: 48105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
;
; APPLICANT: Banerjee, Subhashis
; APPLICANT: Brady, Kenneth D
; APPLICANT: Hodges, John C
; APPLICANT: Kostlan, Catherine R
; APPLICANT: Talanian, Robert V
; TITLE OF INVENTION: N-Substituted Glutamic Acid Derivatives
; TITLE OF INVENTION: with Interleukin-1 Converting Enzyme Inhibitory Activity
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Elizabeth M. Anderson
; STREET: 2800 Plymouth Road
; CITY: Ann Arbor
; STATE: MI
; COUNTRY: US
; ZIP: 48105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Ver 1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,716
; FILING DATE: 13-AUG-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Elizabeth M
; REGISTRATION NUMBER: 31585
; REFERENCE/DOCKET NUMBER: PD-5363-01-EWA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 313 996-7304
; TELEFAX: 313 996-1553
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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; Best Local Similarity 100.0%; Pred. No. 3e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 1 YVAD 4
; Db 1 YVAD 4
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; RESULT 6
; US-08-700-716-16
; Sequence 16, Application US/08700716
; Patent No. 5744451
; GENERAL INFORMATION:
; APPLICANT: Allen, Hamish J
; APPLICANT: Banerjee, Subhashis
; APPLICANT: Brady, Kenneth D
; APPLICANT: Hodges, John C
; APPLICANT: Kostlan, Catherine R
; APPLICANT: Talanian, Robert V
; TITLE OF INVENTION: N-Substituted Glutamic Acid Derivatives
; TITLE OF INVENTION: with Interleukin-1 Converting Enzyme Inhibitory Activity
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Elizabeth M. Anderson
; STREET: 2800 Plymouth Road
; CITY: Ann Arbor
; STATE: MI
; COUNTRY: US
; ZIP: 48105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver 1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,716
FILING DATE: 13-AUG-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Elizabeth M
REGISTRATION NUMBER: 31585
REFERENCE/DOCKET NUMBER: PD-5363-01-EMA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 313 996-7304
TELEFAX: 313 996-1553
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-700-716-16

Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
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Db 1 YVAD 4

RESULT 7
US-08-592-029-4
Sequence 4, Application US/08592029
Patent No. 5763196
GENERAL INFORMATION:
APPLICANT: FOWELL, MICHAEL J.
APPLICANT: KHANNA, PYARE
APPLICANT: LINGENFELTER, DAVID
APPLICANT: EISENBEIS, SCOTT J.
TITLE OF INVENTION: ASSAYS USING CROSS-LINKED POLYPEPTIDE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,029
FILING DATE: 26-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS H.
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 33746-20004.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141 MRSNFOERS SFO
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
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OTHER INFORMATION: /note= "N-methyl aspartic acid"
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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YVAD 4
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Db 1 YVAD 4
RESULT 8
US-08-592-029-5
Sequence 5, Application US/08592029
Patent No. 5763196
GENERAL INFORMATION:
APPLICANT: POWELL, MICHAEL J.
APPLICANT: KHANNA, PYARE
APPLICANT: LINGENFELTER, DAVID
APPLICANT: EISENBEIS, SCOTT J.
TITLE OF INVENTION: ASSAYS USING CROSS-LINKED POLYPEPTIDE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,029
FILING DATE: 26-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS H.
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 33746-20004.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141 MRSNFOERS SFO
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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LOCATION: 4
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OTHER INFORMATION: attached"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1

OTHER INFORMATION: /product= "OTHER"
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OTHER INFORMATION: /note= "Acetyl tyrosine"
US-08-592-029-5
Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YVAD 4
Db 1 YVAD 4
RESULT 9
US-08-777-208-8
Sequence 8, Application US/08777208
Patent No. 5763576
GENERAL INFORMATION:
APPLICANT: Powers, James C.
TITLE OF INVENTION: Tetrapeptide Alpha-Ketoamides
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Deveau, Colton & Marquis
STREET: Two Midtown Plaza, Suite 1400
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,208
FILING DATE: 27-DEC-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/539944
FILING DATE: 06-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colton, Laurence P.
REGISTRATION NUMBER: 33371
REFERENCE/DOCKET NUMBER: 10733-191B
TELEPHONE: (404) 875-3555
TELEFAX: (404) 875-8505
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: no
US-08-777-208-8
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Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YVAD 4
Db 1 YVAD 4
RESULT 10
US-08-800-007A-11
Sequence 11, Application US/08800007A
Patent No. 5834228
GENERAL INFORMATION:
APPLICANT: Becker, Joseph
ADDRESSEE: Nicholson, Donald
STREET: 1251 Avenue of the Americas
APPLICANT: Rotonda, Jennifer
APPLICANT: Thornberry, Nancy
APPLICANT: Fazil, Kimberly
APPLICANT: Gallant, Michel
APPLICANT: Gareau, Yves
APPLICANT: Labelle, Marc
APPLICANT: Peterson, Erin
APPLICANT: Rasper, Dita
TITLE OF INVENTION: CRYSTAL STRUCTURE OF APOPAIN
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: JOSEPH A. COPPOLA - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,007A
FILING DATE: 13-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COPPOLA, JOSEPH A
REGISTRATION NUMBER: 38,413
REFERENCE/DOCKET NUMBER: 19644
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-6734
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRADEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-800-007A-11
Query Match 100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YVAD 4
Db 1 YVAD 4
RESULT 11
US-08-440-898-1
Sequence 1, Application US/08440898
Patent No. 5847135
GENERAL INFORMATION:
APPLICANT: Bemis, Guy W
APPLICANT: Golec, Julian M.C.
APPLICANT: Lauffer, David J
APPLICANT: Mullican, Michael D
APPLICANT: Murcko, Mark A
APPLICANT: Livingston, David J
TITLE OF INVENTION: INHIBITORS OF INTERLEUKIN-1
TITLE OF INVENTION: BETA CONVERTING ENZYME
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr.
STREET: 1251 Avenue of the Americas

STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,898
FILING DATE: 25-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,581
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/261,452
FILING DATE: 17-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: VPI/94-04 CIPRI DIVI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
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NAME/KEY: Modified-site
LOCATION: 1
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OTHER INFORMATION: /note= "tyrosine is succinylated"
FEATURE:
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LOCATION: 4
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OTHER INFORMATION: /note= "aspartic acid residue is derivatized with
OTHER INFORMATION: p-nitroanilide"
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Query Match 100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YVAD 4
DB 1 YVAD 4
RESULT 12
US-08-440-898-2
Sequence 2, Application US/08440898
Patent No. 5847135
GENERAL INFORMATION:
APPLICANT: Bemis, Guy W
APPLICANT: Golec, Julian M.C.
APPLICANT: Lauffer, David J
APPLICANT: Mullican, Michael D
APPLICANT: Murcko, Mark A
APPLICANT: Livingston, David J
TITLE OF INVENTION: INHIBITORS OF INTERLEUKIN-1
TITLE OF INVENTION: BETA CONVERTING ENZYME
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr.

STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,898
FILING DATE: 25-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,581
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/261,452
FILING DATE: 17-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: VPI/94-04 CIPRI DIVI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "tyrosine is acetylated"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "aspartic acid is derivatized with
OTHER INFORMATION: amino-4-methylcoumarin"
US-08-440-898-2
Query Match 100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YVAD 4
DB 1 YVAD 4
RESULT 13
US-08-067-053-1
Sequence 1, Application US/09067053
Patent No. 5932549
GENERAL INFORMATION:
APPLICANT: Allen, Hamish J
APPLICANT: Banerjee, Subhashis
APPLICANT: Brady, Kenneth D
APPLICANT: Hodges, John C
APPLICANT: Kostian, Catherine R
APPLICANT: Talianian, Robert V
TITLE OF INVENTION: N-Substituted Glutamic Acid Derivatives
TITLE OF INVENTION: with Interleukin-1 Converting Enzyme Inhibitory Activity
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:

ADDRESSEE: Elizabeth M. Anderson
STREET: 2800 Plymouth Road
CITY: Ann Arbor
STATE: MI
COUNTRY: US
ZIP: 48105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Ver 1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/067,053
FILING DATE: 27-APR-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/700,716
FILING DATE: 13-AUG-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Elizabeth M
REGISTRATION NUMBER: 31585
REFERENCE/DOCKET NUMBER: PD-5363-01-EVA
TELEPHONE: 313 996-7304
TELEFAX: 313 996-7304
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-067-053-1

Query Match 100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;
OY 1 YVAD 4
DB 1 YVAD 4

RESULT 14
US-09-067-053-16
Sequence 16, Application US/09067053
Patent No. 5932549
GENERAL INFORMATION:
APPLICANT: Allen, Hamish J
APPLICANT: Banerjee, Subhashis
APPLICANT: Brady, Kenneth D
APPLICANT: Hodges, John C
APPLICANT: Kostlan, Catherine R
APPLICANT: Talanian, Robert V
TITLE OF INVENTION: N-Substituted Glutamic Acid Derivatives
TITLE OF INVENTION: with Interleukin-1 Converting Enzyme Inhibitory Activity
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Elizabeth M. Anderson
STREET: 2800 Plymouth Road
CITY: Ann Arbor
STATE: MI
COUNTRY: US
ZIP: 48105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Ver 1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/067,053
FILING DATE: 27-APR-1998

LITING DIV
7500
G083

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/700,716
FILING DATE: 13-AUG-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Elizabeth M
REGISTRATION NUMBER: 31585
REFERENCE/DOCKET NUMBER: PD-5363-01-EVA
TELEPHONE: 313 996-7304
TELEFAX: 313 996-1553
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-067-053-16
Query Match 100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;
OY 1 YVAD 4
DB 1 YVAD 4
RESULT 15
US-09-746-331-10
Sequence 10, Application US/09146331
Patent No. 5958720
GENERAL INFORMATION:
APPLICANT: Litwack, Gerald
APPLICANT: Altmari, Smaad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: Mch2, AN APOPTOTIC CYSTEINE
PROTEASE, AND COMPOSITIONS FOR MAKING AND
METHODS OF USING THE SAME
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
ADDRESSEE: No. 5958720ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/146,331
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/896,885
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TCU-1508
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-146-331-10
Query Match      100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 YVAD 4
Db      1 YVAD 4
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Run on: May 24, 2004, 14:39:37 ; Search time 38 Seconds
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Title: US-09-765-105A-1

Perfect score: 21
Sequence: 1 YVAD 4

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	21	100.0	4	9	US-09-799-463-3
3	21	100.0	4	9	US-09-735-363A-84
4	21	100.0	4	9	US-09-799-994-3
5	21	100.0	4	9	US-09-952-768-72
6	21	100.0	4	9	US-09-150-623-7
7	21	100.0	4	9	US-09-858-754-10
8	21	100.0	4	9	US-09-987-417-2
9	21	100.0	4	9	US-09-977-831-35
10	21	100.0	4	9	US-09-888-243-17
11	21	100.0	4	9	US-09-947-387-2
12	21	100.0	4	9	US-09-964-114-3
13	21	100.0	4	9	US-09-964-114-4
14	21	100.0	4	9	US-09-964-114-6
15	21	100.0	4	10	US-09-161-172-1

16	21	100.0	4	12	US-10-668-955-72	Sequence 72, Appl
17	21	100.0	4	12	US-09-746-731-83	Sequence 83, Appl
18	21	100.0	4	12	US-09-765-105-1	Sequence 1, Appl
19	21	100.0	4	12	US-09-795-651-13	Sequence 13, Appl
20	21	100.0	4	12	US-09-863-649-1	Sequence 1, Appl
21	21	100.0	4	12	US-09-270-983-7	Sequence 7, Appl
22	21	100.0	4	12	US-10-099-408A-1	Sequence 1, Appl
23	21	100.0	4	12	US-09-973-476-2	Sequence 2, Appl
24	21	100.0	4	12	US-10-356-665-2	Sequence 2, Appl
25	21	100.0	4	13	US-10-103-448-7	Sequence 7, Appl
26	21	100.0	4	13	US-10-059-749-83	Sequence 83, Appl
27	21	100.0	4	13	US-10-108-929-7	Sequence 7, Appl
28	21	100.0	4	14	US-10-171-077-10	Sequence 10, Appl
29	21	100.0	4	14	US-10-165-015-35	Sequence 35, Appl
30	21	100.0	4	14	US-10-105-779-2	Sequence 2, Appl
31	21	100.0	4	14	US-10-123-529-26	Sequence 26, Appl
32	21	100.0	4	14	US-10-123-529-28	Sequence 28, Appl
33	21	100.0	4	14	US-10-337-169-27	Sequence 27, Appl
34	21	100.0	4	14	US-10-337-169-30	Sequence 30, Appl
35	21	100.0	4	14	US-10-337-060-16	Sequence 16, Appl
36	21	100.0	4	14	US-10-302-811-3	Sequence 3, Appl
37	21	100.0	4	14	US-10-322-361-1	Sequence 1, Appl
38	21	100.0	4	15	US-10-138-375-2	Sequence 2, Appl
39	21	100.0	4	15	US-10-341-979-12	Sequence 12, Appl
40	21	100.0	5	8	US-08-610-220A-6	Sequence 6, Appl
41	21	100.0	5	9	US-09-150-623-6	Sequence 6, Appl
42	21	100.0	5	9	US-09-954-897-40	Sequence 40, Appl
43	21	100.0	5	9	US-09-947-387-72	Sequence 72, Appl
44	21	100.0	5	10	US-09-997-463B-5	Sequence 5, Appl
45	21	100.0	5	13	US-10-057-505-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-610-220A-7
; Sequence 7, Application US/08610220A
; Publication No. US20030099638A1
; GENERAL INFORMATION:
; APPLICANT: TROY, Carol M.
; TITLE OF INVENTION: COMPOUNDS WHICH PREVENT NEURONAL CELL
; TITLE OF INVENTION: DEATH AND USES THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/610,220A
; FILING DATE: MAR-04-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 48332/JPW/JML
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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; MOLECULE TYPE: peptide
US-08-610-220A-7
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Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YVAD 4
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Db      1 YVAD 4

RESULT 2
US-09-799-463-3
; Sequence 3, Application US/09799463
; Patent No. US20010018195A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Deveraux, Quinn
; APPLICANT: Salvessen, Guy S.
; APPLICANT: Takahashi, Ryosuke
; APPLICANT: Roy, Natalie
; TITLE OF INVENTION: Screening Assays For Agents That Alter Inhibitor of
; FILE REFERENCE: LJ 3080
; CURRENT APPLICATION NUMBER: US/09/799,463
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 09/058,969
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 08/862,087
; PRIOR FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Consensus Sequence
US-09-799-463-3

Query Match      100.0%; Score 21; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YVAD 4
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Db      1 YVAD 4

RESULT 3
US-09-735-363A-84
; Sequence 84, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillon, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 84
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide

US-09-735-363A-84
Query Match      100.0%; Score 21; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YVAD 4
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Db      1 YVAD 4

RESULT 4
US-09-799-994-3
; Sequence 3, Application US/09799994
; Patent No. US20020009757A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Deveraux, Quinn
; APPLICANT: Salvessen, Guy S.
; APPLICANT: Takahashi, Ryosuke
; APPLICANT: Roy, Natalie
; TITLE OF INVENTION: Screening Assays For Agents That Alter Inhibitor of
; FILE REFERENCE: LJ 3080
; CURRENT APPLICATION NUMBER: US/09/799,994
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 09/058,969
; PRIOR FILING DATE: 1998-04-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Consensus Sequence
US-09-799-994-3

Query Match      100.0%; Score 21; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YVAD 4
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Db      1 YVAD 4

RESULT 5
US-09-952-768-72
; Sequence 72, Application US/09952768
; Patent No. US20020035242A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; APPLICANT: Armstrong, Robert
; APPLICANT: Tomaselli, Kevin
; TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE,
; FILE REFERENCE: NUCLEIC ACIDS ENCODING AND METHODS OF USE
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: Suite 6300, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/09/952,768
FILING DATE: 10-Sep-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Christiansen, William T.
REGISTRATION NUMBER: 44,614
REFERENCE/DOCKET NUMBER: 480140.424C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 72:

US-09-952-768-72

Query Match 100.0%; Score 21; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
DB 1 YVAD 4

RESULT 6

US-09-150-623-7
Sequence 7, Application US/09150623
Patent No. US20020044931A1
GENERAL INFORMATION:
APPLICANT: Troy, Carol M.
TITLE OF INVENTION: COMPOUNDS WHICH PREVENT NEURONAL CELL
TITLE OF INVENTION: DEATH AND USES THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/150,623
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/610,220
FILING DATE: MAR-04-1996
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 48332/JPW/JML
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-09-150-623-7

Query Match 100.0%; Score 21; DB 9; Length 4;

Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
DB 1 YVAD 4

RESULT 7

US-09-858-754-10
Sequence 10, Application US/09858754
Patent No. US20020055130A1
GENERAL INFORMATION:
APPLICANT: Johnson, Gary L.
TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING APOPTOSIS
FILE REFERENCE: CPI-042
CURRENT APPLICATION NUMBER: US/09/858,754
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/023,130
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: 60/039,740
PRIOR FILING DATE: 1997-02-14
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 10
LENGTH: 4
TYPE: PRT
ORGANISM: synthetic construct
US-09-858-754-10

Query Match 100.0%; Score 21; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
DB 1 YVAD 4

RESULT 8

US-09-987-417-2
Sequence 2, Application US/09987417
Patent No. US20020058631A1
GENERAL INFORMATION:
APPLICANT: Cai, Sui Xiong
APPLICANT: Weber, Eckard
APPLICANT: Wang, Yan
APPLICANT: Mills, Gordon B.
APPLICANT: Green, Douglas R.
TITLE OF INVENTION: Caspase Inhibitors and the Use Thereof
FILE REFERENCE: 1735.0350003
CURRENT APPLICATION NUMBER: US/09/987,417
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 09/545,565
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: US 60/128,545
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: US 60/158,370
PRIOR FILING DATE: 1999-10-12
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 2
LENGTH: 4
TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: caspase-1 inhibitor
US-09-987-417-2

Query Match 100.0%; Score 21; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
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 Db 1 YVAD 4

RESULT 9

US-09-977-831-35
 ; Sequence 35, Application US/09977831
 ; Patent No. US20020120100A1
 ; GENERAL INFORMATION:
 ; APPLICANT: PACIT, Tech Transfer Office University of Lausanne
 ; APPLICANT: Bonny, Christophe
 ; TITLE OF INVENTION: INTRACELLULAR DELIVERY OF BIOLOGICAL EFFECTORS
 ; FILE REFERENCE: 20349-512 Transporter peptides
 ; CURRENT APPLICATION NUMBER: US/09/977,831
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: U.S.S.N. 60/240,315
 ; PRIOR FILING DATE: 2000-10-13
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 35
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Caspase
 ; OTHER INFORMATION: Inhibitor peptide
 ; US-09-977-831-35

Query Match 100.0%; Score 21; DB 9; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
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 Db 1 YVAD 4

RESULT 10

US-09-888-243-17
 ; Sequence 17, Application US/09888243
 ; Patent No. US20020136714A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Horvitz, H. Robert
 ; APPLICANT: Yuan, Junying
 ; APPLICANT: Shaham, Shai
 ; TITLE OF INVENTION: Relatedness of Human Interleukin-1beta
 ; TITLE OF INVENTION: Convertase Gene to a C. Elegans Cell Death Gene, Inhibitory
 ; TITLE OF INVENTION: Portions of these Genes and Uses Therefor
 ; FILE REFERENCE: 01997/211003
 ; CURRENT APPLICATION NUMBER: US/09/888,243
 ; CURRENT FILING DATE: 2001-05-22
 ; PRIOR APPLICATION NUMBER: US 09/083,662
 ; PRIOR FILING DATE: 1998-05-22
 ; PRIOR APPLICATION NUMBER: US 08/394,189
 ; PRIOR FILING DATE: 1995-02-24
 ; PRIOR APPLICATION NUMBER: US 08/282,211
 ; PRIOR FILING DATE: 1994-07-11
 ; PRIOR APPLICATION NUMBER: US 07/984,182
 ; PRIOR FILING DATE: 1992-11-20
 ; PRIOR APPLICATION NUMBER: US 07/897,788
 ; PRIOR FILING DATE: 1992-06-12
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 17
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Designed Peptide
 ; US-09-888-243-17

Query Match 100.0%; Score 21; DB 9; Length 4;

Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
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 Db 1 YVAD 4

RESULT 11

US-09-947-387-2
 ; Sequence 2, Application US/09947387
 ; Patent No. US20020150895A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Weber, Eckard
 ; APPLICANT: Cai, Sui Xiong
 ; APPLICANT: Keana, John F.W.
 ; APPLICANT: Drewe, John A.
 ; APPLICANT: Zhang, Han-Zhong
 ; TITLE OF INVENTION: No. US20020150895A1el Fluorogenic or Fluorescent Reporter Molecu
 ; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
 ; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
 ; TITLE OF INVENTION: Use thereof
 ; FILE REFERENCE: 1735.0290005
 ; CURRENT APPLICATION NUMBER: US/09/947,387
 ; CURRENT FILING DATE: 2001-09-07
 ; PRIOR APPLICATION NUMBER: US 60/061,582
 ; PRIOR FILING DATE: 1997-10-10
 ; PRIOR APPLICATION NUMBER: US 60/145,746
 ; PRIOR FILING DATE: 1998-03-03
 ; PRIOR APPLICATION NUMBER: US 09/168,888
 ; PRIOR FILING DATE: 1998-10-09
 ; NUMBER OF SEQ ID NOS: 142
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: Peptide
 ; US-09-947-387-2

Query Match 100.0%; Score 21; DB 9; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
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 Db 1 YVAD 4

RESULT 12

US-09-964-114-3
 ; Sequence 3, Application US/09964114
 ; Patent No. US20020156094A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Albrecht, Hans P. et al.
 ; TITLE OF INVENTION: Sulfonamide Interleukin-1beta Converting Enzyme
 ; TITLE OF INVENTION: Inhibitors
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/09/964,114
 ; CURRENT FILING DATE: 2001-09-25
 ; PRIOR APPLICATION NUMBER: 09/284,422
 ; PRIOR FILING DATE: 1999-04-02
 ; PRIOR APPLICATION NUMBER: PCT/US97/18396
 ; PRIOR FILING DATE: 1999-10-09
 ; PRIOR APPLICATION NUMBER: 60/028,313
 ; PRIOR FILING DATE: 1996-10-11
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 4
 ; TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: UNSURE
LOCATION: (1)..(4)
OTHER INFORMATION: Acetyl group attached to 5' end and AWC group
OTHER INFORMATION: attached to 3' end
OTHER INFORMATION: Description of Artificial Sequence: Chemically
OTHER INFORMATION: synthesized
US-09-964-114-3

Query Match 100.0%; Score 21; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
|||
Db 1 YVAD 4

RESULT 13
US-09-964-114-4
Sequence 4, Application US/09964114
Patent No. US20020156094A1
GENERAL INFORMATION:
APPLICANT: Albrecht, Hans P. et al.
TITLE OF INVENTION: Sulfonamide Interleukin-1Beta Converting Enzyme
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/964,114
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/284,422
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: PCT/US97/18396
PRIOR FILING DATE: 1999-10-09
PRIOR APPLICATION NUMBER: 60/028,313
PRIOR FILING DATE: 1998-10-11
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 4
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: UNSURE
LOCATION: (1)..(4)
OTHER INFORMATION: Acetyl group attached to 5' end and pNA group
OTHER INFORMATION: attached to 3' end
OTHER INFORMATION: Description of Artificial Sequence: Chemically
OTHER INFORMATION: synthesized
US-09-964-114-4

Query Match 100.0%; Score 21; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
|||
Db 1 YVAD 4

RESULT 14
US-09-964-114-6
Sequence 6, Application US/09964114
Patent No. US20020156094A1
GENERAL INFORMATION:
APPLICANT: Albrecht, Hans P. et al.
TITLE OF INVENTION: Sulfonamide Interleukin-1Beta Converting Enzyme
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/964,114
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/284,422
PRIOR FILING DATE: 1999-04-02

PRIOR APPLICATION NUMBER: PCT/US97/18396
PRIOR FILING DATE: 1999-10-09
PRIOR APPLICATION NUMBER: 60/028,313
PRIOR FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 6
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: UNSURE
LOCATION: (1)..(4)
OTHER INFORMATION: Acetyl group attached to 5' end and pNA group
OTHER INFORMATION: attached to 3' end
OTHER INFORMATION: Description of Artificial Sequence: Chemically
OTHER INFORMATION: synthesized
US-09-964-114-6

Query Match 100.0%; Score 21; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
|||
Db 1 YVAD 4

RESULT 15
US-09-161-172-1
Sequence 1, Application US/09161172
Publication No. US20030044776A1
GENERAL INFORMATION:
APPLICANT: Dykens, James A.
APPLICANT: Miller, Scott W.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
TITLE OF INVENTION: AGENTS THAT ALTER MITOCHONDRIAL PERMEABILITY
TITLE OF INVENTION: TRANSITION PORES
FILE REFERENCE: 660088.418
CURRENT APPLICATION NUMBER: US/09/161,172
CURRENT FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: caspase-1 specific fluorogenic peptide substrate
US-09-161-172-1

Query Match 100.0%; Score 21; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
|||
Db 1 YVAD 4

Search completed: May 24, 2004, 14:49:50
Job time : 39 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 24, 2004, 14:38:22 ; Search time 175 Seconds
(without alignments)
22.310 Million cell updates/sec

Title: US-09-765-105A-1
Perfect score: 21
Sequence: 1 YVAD 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6019581 seqs, 976053577 residues

Total number of hits satisfying chosen parameters: 6019581

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA Main:

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- 10: /cgn2_6/ptodata/2/paa/US086 COMB.pcp.*
- 11: /cgn2_6/ptodata/2/paa/US087 COMB.pcp.*
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- 24: /cgn2_6/ptodata/2/paa/US099A COMB.pcp.*
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- 28: /cgn2_6/ptodata/2/paa/US102 COMB.pcp.*
- 29: /cgn2_6/ptodata/2/paa/US103 COMB.pcp.*
- 30: /cgn2_6/ptodata/2/paa/US104 COMB.pcp.*
- 31: /cgn2_6/ptodata/2/paa/US106 COMB.pcp.*
- 32: /cgn2_6/ptodata/2/paa/US107 COMB.pcp.*
- 33: /cgn2_6/ptodata/2/paa/US60 COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description

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2	21	100.0	4	1	PCT-US01-04137-2	Sequence 2, Appli
3	21	100.0	4	1	PCT-US01-04137-3	Sequence 3, Appli
4	21	100.0	4	1	PCT-US02-18014-9	Sequence 9, Appli
5	21	100.0	4	1	PCT-US02-18484-9	Sequence 9, Appli
6	21	100.0	4	1	PCT-US02-37577-3	Sequence 3, Appli
7	21	100.0	4	1	PCT-US03-20997-7	Sequence 7, Appli
8	21	100.0	4	1	PCT-US96-07010-10	Sequence 10, Appli
9	21	100.0	4	1	PCT-US98-12716-28	Sequence 26, Appli
10	21	100.0	4	1	PCT-US98-12716-28	Sequence 28, Appli
11	21	100.0	4	1	PCT-US98-21231-2	Sequence 2, Appli
12	21	100.0	4	1	PCT-US99-08064-36	Sequence 36, Appli
13	21	100.0	4	1	PCT-US99-16423-2	Sequence 2, Appli
14	21	100.0	4	5	US-08-183-269-1	Sequence 1, Appli
15	21	100.0	4	6	US-08-282-211A-16	Sequence 16, Appli
16	21	100.0	4	7	US-08-391-674-17	Sequence 17, Appli
17	21	100.0	4	8	US-08-463-080-17	Sequence 17, Appli
18	21	100.0	4	11	US-08-768-448-2	Sequence 2, Appli
19	21	100.0	4	11	US-08-768-448-3	Sequence 3, Appli
20	21	100.0	4	11	US-08-768-448-5	Sequence 5, Appli
21	21	100.0	4	11	US-08-768-448-9	Sequence 9, Appli
22	21	100.0	4	11	US-08-768-448-13	Sequence 13, Appli
23	21	100.0	4	11	US-08-768-448-16	Sequence 16, Appli
24	21	100.0	4	11	US-08-768-448-17	Sequence 17, Appli
25	21	100.0	4	13	US-08-902-766-4	Sequence 4, Appli
26	21	100.0	4	13	US-08-902-766-5	Sequence 5, Appli
27	21	100.0	4	13	US-08-902-766-10	Sequence 10, Appli
28	21	100.0	4	13	US-08-918-674-3	Sequence 3, Appli
29	21	100.0	4	13	US-08-948-124-2	Sequence 2, Appli
30	21	100.0	4	14	US-09-023-130-10	Sequence 10, Appli
31	21	100.0	4	14	US-09-026-715-2	Sequence 2, Appli
32	21	100.0	4	14	US-09-083-663-16	Sequence 16, Appli
33	21	100.0	4	14	US-09-083-663-17	Sequence 17, Appli
34	21	100.0	4	14	US-09-099-463-26	Sequence 26, Appli
35	21	100.0	4	14	US-09-099-463-28	Sequence 28, Appli
36	21	100.0	4	14	US-09-099-463A-26	Sequence 26, Appli
37	21	100.0	4	14	US-09-099-463A-28	Sequence 28, Appli
38	21	100.0	4	15	US-09-150-623-7	Sequence 7, Appli
39	21	100.0	4	15	US-09-161-172-1	Sequence 1, Appli
40	21	100.0	4	16	US-09-270-983-7	Sequence 7, Appli
41	21	100.0	4	16	US-09-296-662-26	Sequence 26, Appli
42	21	100.0	4	16	US-09-296-662B-26	Sequence 26, Appli
43	21	100.0	4	17	US-09-336-951B-2	Sequence 2, Appli
44	21	100.0	4	17	US-09-380-546-13	Sequence 13, Appli
45	21	100.0	4	17	US-09-380-546A-11	Sequence 11, Appli

ALIGNMENTS

RESULT 1
PCT-US00-09319-2
; Sequence 2, Application PC/TUS0009319
; GENERAL INFORMATION:
; APPLICANT: Cytovia, Inc.
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Weber, Eckard
; APPLICANT: Wang, Yan
; APPLICANT: Mills, Gordon B.
; APPLICANT: Green, Douglas R.
; TITLE OF INVENTION: Caspase Inhibitors and the Use Thereof
; FILE REFERENCE: 1735-035PC02
; CURRENT APPLICATION NUMBER: PCT/US00/09319
; CURRENT FILING DATE: 2000-04-07
; EARLIER APPLICATION NUMBER: US 60/128,545
; EARLIER FILING DATE: 1999-04-09
; EARLIER APPLICATION NUMBER: US 60/158,370
; EARLIER FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT

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; ORGANISM: Unknown Organism
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; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: caspase-1
; OTHER INFORMATION: inhibitor
PCT-US00-09319-2

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Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred.No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels

QY	1	YVAD	4
Db	1	YVAD	4

RESULT 2

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PCT/US01-04137-2
; Sequence 2: Application PC/TUS0104137
; GENERAL INFORMATION:
; APPLICANT: ALEXION PHARMACEUTICALS, INC.
; APPLICANT: FCGOR, William L.
; TITLE OF INVENTION: MIXTURES OF CASPASE INHIBITORS AND COMPLEMENT
; TITLE OF INVENTION: INHIBITORS AND METHODS OF USE THEREOF
; FILE REFERENCE: 1087-15PCT
; CURRENT APPLICATION NUMBER: PCT/US01/04137
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2

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TYPE: PKI
ORGANISM: Artificial Sequence

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; ORGANISM: Artificial Sequence
;
; FEATURE:
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; OTHER INFORMATION: Description of Artificial Sequence: Caspase
; OTHER INFORMATION: inhibitor
PCT-US01-04137-2

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Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. NO. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels

QY	1	YVAD	4
DB	1	YVAD	4

RESULT 3

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PCT-US01-04137-3
:
: Sequence 3, Application PC/TUS0104137
: GENERAL INFORMATION:
:
: APPLICANT: ALEXION PHARMACEUTICALS, INC.
: APPLICANT: Fodor, William L.
: TITLE OF INVENTION: MIXTURES OF CASPASE INHIBITORS AND COMPLEMENT
: TITLE OF INVENTION: INHIBITORS AND METHODS OF USE THEREOF
:
: FILE REFERENCE: 1087-15PCT
: CURRENT APPLICATION NUMBER: PCT/US01/04137
: CURRENT FILING DATE: 2001-05-09
: NUMBER OF SEQ ID NOS: 3
: SOFTWARE: PatentIn Ver. 2.1
:

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; LENGTH: 4

; TYPE: PRT

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Caspase
; OTHER INFORMATION: inhibitor
PCT-US01-04137-3

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Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels

QY 1 YVAD 4

1 YVAD 4

RESULT 4

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PCT-US02-18014-9
; Sequence 9, Application PC/TUS0218014
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Rechsteiner, Martin
; APPLICANT: Pratt, Gregory
; APPLICANT: Li, Jun
; TITLE OF INVENTION: METHODS FOR IDENTIFYING COMPOUNDS WITH
; THERAPEUTIC POTENTIAL FOR TREATMENT OF CENTRAL
; NERVOUS SYSTEM DEGENERATIVE DISEASES RESULTING FROM ABNORMAL PROTEIN
; METABOLISM
; TITLE OF INVENTION: NEURODEGENERATIVE DISEASES RESULTING FROM ABNORMAL PROTEIN
; METABOLISM
; TITLE OF INVENTION: OR PEPTIDE ACCUMULATION
; FILE REFERENCE: 21101.0013P1
; CURRENT APPLICATION NUMBER: PCT/US02/18014
; CURRENT FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/297,332
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: note =
; OTHER INFORMATION: synthetic construct
PCT-US02-18014-9

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Query Match      100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels
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Qy	1	YVAD	4
Dy	1	YVAD	4

RESULT 5

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PCT-US02-18484-9
; Sequence 9, Application PC/TUS0218484
; GENERAL INFORMATION:
; APPLICANT: Mitokor
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: ORGANELLAR PROTEOMES INCLUDING
; TITLE OF INVENTION: DETERMINATION OF TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME USING MASS
; TITLE OF INVENTION: SPECTROMETRY
; FILE REFERENCE: 660088.450PC
; CURRENT APPLICATION NUMBER: PCT/US02/18484
; CURRENT FILING DATE: 2002-06-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)...(1)
; OTHER INFORMATION: Benzoyl carbonyl moiety
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)...(4)
; OTHER INFORMATION: 7-amino-4-trifluoromethylcoumarin
PCT-US02-18484-9

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Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
DB 1 YVAD 4

RESULT 6
PCT-US02-37577-3
; Sequence 3, Application PC/TUS0237577
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Reed, John C.
; APPLICANT: Houghten, Richard A.
; APPLICANT: Nefzi, Adel
; APPLICANT: Ostresh, John M.
; APPLICANT: Pinilla, Clemencia
; APPLICANT: Welsh, Kate
; TITLE OF INVENTION: Methods and Compositions for
; TITLE OF INVENTION: Derepression of IAP-Inhibited Caspase
; FILE REFERENCE: FP-LJ 5449
; CURRENT APPLICATION NUMBER: PCT/US02/37577
; CURRENT FILING DATE: 2002-11-21
; PRIOR FILING DATE: 2001-11-21
; PRIOR FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
PCT-US02-37577-3

Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
DB 1 YVAD 4

RESULT 7
PCT-US03-20997-7
; Sequence 7, Application PC/TUS0320997
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Wade, EDRIS
; TITLE OF INVENTION: CASPASE 9 ACTIVATION AND USES THEREFOR
; FILE REFERENCE: AM101006 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/20997
; CURRENT FILING DATE: 2003-07-08
; PRIOR FILING DATE: 2003-07-08
; PRIOR FILING DATE: 2002-07-08
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Substrate
PCT-US03-20997-7

Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
DB 1 YVAD 4

RESULT 8
PCT-US96-07010-10
; Sequence 10, Application PC/TUS9607010
; GENERAL INFORMATION:
; APPLICANT: Litwack, Gerald
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: Mch2, AN APOPTOTIC CYSTEINE
; TITLE OF INVENTION: PROTEASE, AND COMPOSITIONS FOR
; TITLE OF INVENTION: MAKING AND METHODS OF USING THE
; TITLE OF INVENTION: SAME
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
; ADDRESSEE: Norris
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/07010
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/446,925
; FILING DATE: 18-MAY-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1882
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-07010-10

Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
DB 1 YVAD 4

RESULT 9
PCT-US98-12716-26
; Sequence 26, Application PC/TUS9812716
; GENERAL INFORMATION:
; APPLICANT: Yuan, Junying
; APPLICANT: Friedlander, Robert M.
; TITLE OF INVENTION: Interleukin Converting Enzyme (ICE)
; TITLE OF INVENTION: and Central Nervous System Damage
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
PCT-US98-12716-26

STREET: 1100 New York Avenue NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/12716
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/050,242
FILING DATE: 19-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Jorge A. Goldstein
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609.442PC01/JAG/LBB
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /label= Ac
OTHER INFORMATION: /note= "An acetyl (Ac) group is attached to the tyrosine residue."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /label= CHO
OTHER INFORMATION: /note= "An aldehyde (CHO) is attached to the C-terminal aspartic acid residue."
PCT-US98-12716-26

Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
|||
Db 1 YVAD 4

RESULT 10
PCT-US98-12716-28
Sequence 28, Application PC/TUS9812716
GENERAL INFORMATION:
APPLICANT: Yuan, Junying
APPLICANT: Friedlander, Robert M.
TITLE OF INVENTION: Interleukin Converting Enzyme (ICE)
TITLE OF INVENTION: Interleukin Converting Enzyme (ICE)
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

STREET: 1100 New York Avenue NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/12716
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/050,242
FILING DATE: 19-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Jorge A. Goldstein
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609.442PC01/JAG/LBB
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /label= Ac
OTHER INFORMATION: /note= "An acetyl (Ac) group is attached to the tyrosine residue."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /label= CHO
OTHER INFORMATION: /note= "An aldehyde (CHO) is attached to the C-terminal aspartic acid residue."
PCT-US98-12716-28

Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
|||
Db 1 YVAD 4

RESULT 11
PCT-US98-21231-2
Sequence 2, Application PC/TUS9821231
GENERAL INFORMATION:
APPLICANT: Cytovia, Inc.
TITLE OF INVENTION: Novel Fluorogenic or Fluorescent Reporter Molecules and
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: Use Thereof
FILE REFERENCE: 1735.029PC02
CURRENT APPLICATION NUMBER: PCT/US98/21231
CURRENT FILING DATE: 1998-10-09
EARLIER APPLICATION NUMBER: US 60/061,592
EARLIER FILING DATE: 1997-10-10
EARLIER APPLICATION NUMBER: US 09/033,661
EARLIER FILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 142
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Peptide
PCT-US98-21231-2

Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
Db 1 YVAD 4

RESULT 12

PCT-US99-08064-36
Sequence 36, Application PC/TUS9908064A

GENERAL INFORMATION:

APPLICANT: Yuan, Junying
APPLICANT: Morishima, Nobuhito
APPLICANT: The General Hospital Corporation
TITLE OF INVENTION: Programmed Cell Death and Caspase-12

FILE REFERENCE: 0609.440PC01

CURRENT APPLICATION NUMBER: PCT/US99/08064A

CURRENT FILING DATE: 1999-04-14

EARLIER APPLICATION NUMBER: US 60/081,962

EARLIER FILING DATE: 1998-04-16

NUMBER OF SEQ ID NOS: 38

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 36

LENGTH: 4

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Peptide

OTHER INFORMATION: Inhibitor

PCT-US99-08064-36

Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
Db 1 YVAD 4

RESULT 13

PCT-US99-16423-2

Sequence 2, Application PC/TUS9916423

GENERAL INFORMATION:

APPLICANT: Cytovia, Inc.

APPLICANT: Zhang, Han-Zhong

APPLICANT: Cai, Sui Xiong

APPLICANT: Drewe, John A.

APPLICANT: Yang, Wu

TITLE OF INVENTION: Novel Fluorescence Dyes and Their Applications for Whole-Cell

TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Proteases

TITLE OF INVENTION: Other Enzymes and the Use Thereof

FILE REFERENCE: 1735.003PC01

CURRENT APPLICATION NUMBER: PCT/US99/16423

CURRENT FILING DATE: 1999-07-21

EARLIER APPLICATION NUMBER: US 60/093,642

EARLIER FILING DATE: 21-JUL-1998

NUMBER OF SEQ ID NOS: 139

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 4

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Peptide

PCT-US99-16423-2

Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
Db 1 YVAD 4

RESULT 14

US-08-183-269-1

Sequence 1, Application US/08183269

GENERAL INFORMATION:

APPLICANT: Molineaux, Susan M.

APPLICANT: Rolando, Anna M.

APPLICANT: Casano, Francesca J.

TITLE OF INVENTION: DNA Encoding Murine Precursor

TITLE OF INVENTION: Interleukin 1 Beta Converting Enzyme

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merck & Co., Inc.

STREET: P.O. Box 2000

CITY: Rahway

STATE: NJ

COUNTRY: USA

ZIP: 07065

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/183,269

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/947,330

FILING DATE: 18-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Wallen, John W.

REGISTRATION NUMBER: 35,403

REFERENCE/DOCKET NUMBER: 18857

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 594-3905

TELEFAX: (908) 594-4720

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-183-269-1

Query Match 100.0%; Score 21; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
Db 1 YVAD 4

RESULT 15

US-08-282-211A-16

Sequence 16, Application US/08282211A

GENERAL INFORMATION:

APPLICANT: Horvitz, H. Robert

APPLICANT: Yuan, Junying

APPLICANT: Shaham, Shai

TITLE OF INVENTION: RELATEDNESS OF HUMAN INTERLEUKIN-1

TITLE OF INVENTION: CONVERTASE GENE TO A C. ELEGANS CELL DEATH GENE,

TITLE OF INVENTION: INHIBITORY PORTIONS OF THESE GENES AND USES THEREFOR

; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/282.211A
; FILING DATE: 11-JUL-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 01997/198004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-282-211A-16

Query Match 100.0%; Score 21; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
DB 1 YVAD 4

Search completed: May 24, 2004, 14:47:41
Job time : 176 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 24, 2004, 14:39:07 ; Search time 13.5 Seconds
(without alignments)

10.992 Million cell updates/sec

Title: US-09-765-105A-1

Perfect score: 21

Sequence: 1 YVAD 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 251736 seqs, 37097828 residues

Total number of hits satisfying chosen parameters: 251736

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New:*

- 1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep.*
- 2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
- 7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	21	100.0	4	1	PCT-US03-41600-528
2	21	100.0	4	6	US-10-627-556-528
3	21	100.0	4	6	US-10-630-926-15
4	21	100.0	4	6	US-10-829-381-2
5	21	100.0	4	6	US-10-665-668A-7
6	21	100.0	5	6	US-10-823-381-72
7	21	100.0	5	6	US-10-663-668A-6
8	21	100.0	6	6	US-10-829-381-142
9	21	100.0	14	5	US-09-394-019B-42
10	21	100.0	14	5	US-09-394-019B-43
11	21	100.0	14	5	US-09-394-019B-287
12	21	100.0	14	5	US-09-394-019B-288
13	21	100.0	14	5	US-09-394-019B-42
14	21	100.0	14	5	US-09-394-019B-43
15	21	100.0	14	5	US-09-394-019C-42
16	21	100.0	14	5	US-09-394-019C-43
17	21	100.0	14	5	US-09-394-019C-287
18	21	100.0	14	5	US-09-394-019C-288
19	21	100.0	16	5	US-09-394-019B-45
20	21	100.0	16	5	US-09-394-019B-46
21	21	100.0	16	5	US-09-394-019B-290
22	21	100.0	16	5	US-09-394-019B-291
23	21	100.0	16	5	US-09-394-019B-45
24	21	100.0	16	5	US-09-394-019B-46
25	21	100.0	16	5	US-09-394-019C-45
26	21	100.0	16	5	US-09-394-019C-46

27 21 100.0 16 5 US-09-394-019C-290 Sequence 290, App
28 21 100.0 16 5 US-09-394-019C-291 Sequence 291, App
29 21 100.0 18 5 US-09-394-019B-48 Sequence 48, Appl
30 21 100.0 18 5 US-09-394-019B-51 Sequence 51, Appl
31 21 100.0 18 5 US-09-394-019B-52 Sequence 52, Appl
32 21 100.0 18 5 US-09-394-019B-293 Sequence 293, App
33 21 100.0 18 5 US-09-394-019B-296 Sequence 296, App
34 21 100.0 18 5 US-09-394-019B-297 Sequence 297, App
35 21 100.0 18 5 US-09-394-019B-48 Sequence 48, Appl
36 21 100.0 18 5 US-09-394-019B-51 Sequence 51, Appl
37 21 100.0 18 5 US-09-394-019B-52 Sequence 52, Appl
38 21 100.0 18 5 US-09-394-019C-48 Sequence 48, Appl
39 21 100.0 18 5 US-09-394-019C-51 Sequence 51, Appl
40 21 100.0 18 5 US-09-394-019C-52 Sequence 52, Appl
41 21 100.0 18 5 US-09-394-019C-293 Sequence 293, App
42 21 100.0 18 5 US-09-394-019C-296 Sequence 296, App
43 21 100.0 18 5 US-09-394-019C-297 Sequence 297, App
44 21 100.0 41 6 US-10-100-683-8636 Sequence 8636, Ap
45 21 100.0 65 6 US-10-417-884A-6345 Sequence 6345, Ap

ALIGNMENTS

RESULT 1
PCT-US03-41600-528
; Sequence 528, Application PC/TUS0341600
; GENERAL INFORMATION:
; APPLICANT: TRIBION PHARMACEUTICALS, INC.
; TITLE OF INVENTION: BINDING CONSTRUCTS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 49076.000004.CIP3PCT
; CURRENT APPLICATION NUMBER: PCT/US03/41600
; CURRENT FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: 10/627,556
; PRIOR FILING DATE: 2003-07-26
; NUMBER OF SEQ ID NOS: 699
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 528
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
PCT-US03-41600-528

Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4

Db 1 YVAD 4

RESULT 2
US-10-627-556-528
; Sequence 528, Application US/10627556
; GENERAL INFORMATION:
; APPLICANT: LEDBETTER, JEFFREY A.
; APPLICANT: HAYDEN-LEDBETTER, MARTHA
; APPLICANT: THOMPSON, PETER A.
; TITLE OF INVENTION: BINDING CONSTRUCTS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 49076.000004.CIP2
; CURRENT APPLICATION NUMBER: US/10/627,556
; CURRENT FILING DATE: 2003-07-26
; PRIOR APPLICATION NUMBER: 10/053,530
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/367,358
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/765,208
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/385,691

;; PRIOR FILING DATE: 2002-06-03
;; NUMBER OF SEQ ID NOS: 699
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 528
;; LENGTH: 4
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;; OTHER INFORMATION: peptide
US-10-627-556-528

Query Match 100.0%; Score 21; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
Db 1 YVAD 4

RESULT 3
US-10-630-926-15
; Sequence 15, Application US/10630926
; GENERAL INFORMATION:
; APPLICANT: RICCARDI, Carlo
; TITLE OF INVENTION: INTRACELLULAR MODULATORS OF APOPTIC CELL
; DEATH PATHWAYS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 624 Ninth Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/630,926
; FILING DATE: 31-Jul-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/403,861A
; FILING DATE: 11-Feb-2000
; APPLICATION NUMBER: PCT/EP98/02490
; FILING DATE: 27-APR-1998
; APPLICATION NUMBER: EP 97107033.9
; FILING DATE: 28-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: RICCARDI=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: /note= "the N-terminus is modified by an
; acetyl group; the C-terminus is modified with CH2OC(O)-[2,6-(CF3)2]Ph"
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-630-926-15

Query Match 100.0%; Score 21; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
Db 1 YVAD 4

RESULT 4
US-10-829-381-2
; Sequence 2, Application US/10829381
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: Novel Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290006
; CURRENT APPLICATION NUMBER: US/10/829,381
; CURRENT FILING DATE: 2004-04-22
; PRIOR APPLICATION NUMBER: US 60/061,582
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: US 60/145,746
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: US 09/168,888
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: US 09/947,387
; PRIOR FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-829-381-2

Query Match 100.0%; Score 21; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
Db 1 YVAD 4

RESULT 5
US-10-665-668A-7
; Sequence 7, Application US/1065668A
; GENERAL INFORMATION:
; APPLICANT: TROY, CAROL M.
; TITLE OF INVENTION: COMPOUNDS WHICH PREVENT CELL DEATH AND USES THEREOF
; FILE REFERENCE: 0575/48332-B
; CURRENT APPLICATION NUMBER: US/10/665,668A
; CURRENT FILING DATE: 2003-09-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 4
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MOTIF OF PSEUDOSUBSTRATE INHIBITOR
US-10-665-668A-7

Query Match 100.0%; Score 21; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
|||
Db 1 YVAD 4

RESULT 6
US-10-829-381-72
; Sequence 72, Application US/10829381
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: Novel Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290006
; CURRENT APPLICATION NUMBER: US/10/829,381
; CURRENT FILING DATE: 2004-04-22
; PRIOR APPLICATION NUMBER: US 60/061,582
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: US 60/145,746
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: US 09/168,888
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: US 09/947,387
; PRIOR FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-10-829-381-72

Query Match 100.0%; Score 21; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
|||
Db 1 YVAD 4

RESULT 7
US-10-665-668A-6
; Sequence 6, Application US/10665668A
; GENERAL INFORMATION:
; APPLICANT: TROY, CAROL M.
; TITLE OF INVENTION: COMPOUNDS WHICH PREVENT CELL DEATH AND USES THEREOF
; FILE REFERENCE: 0575/48332-B
; CURRENT APPLICATION NUMBER: US/10/665,668A
; CURRENT FILING DATE: 2003-09-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 5
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: COMPETITIVE INHIBITOR OF ICE
US-10-665-668A-6

Query Match 100.0%; Score 21; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4

Db 2 YVAD 5
|||

RESULT 8
US-10-829-381-142
; Sequence 142, Application US/10829381
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: Novel Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290006
; CURRENT APPLICATION NUMBER: US/10/829,381
; CURRENT FILING DATE: 2004-04-22
; PRIOR APPLICATION NUMBER: US 60/061,582
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: US 60/145,746
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: US 09/168,888
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: US 09/947,387
; PRIOR FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 142
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-10-829-381-142

Query Match 100.0%; Score 21; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
|||
Db 1 YVAD 4

RESULT 9
US-09-394-019B-42
; Sequence 42, Application US/09394019B
; GENERAL INFORMATION:
; APPLICANT: Oncoimmun, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
; TITLE OF INVENTION: SAMPLES AND METHODS OF USE THEREOF
; FILE REFERENCE: 300-903820US
; CURRENT APPLICATION NUMBER: US/09/394,019B
; CURRENT FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide substrate
; FEATURE:

```
; NAME/KEY: MOD_RES
; LOCATION: (3)..(3)
; OTHER INFORMATION: X is Alb
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-394-019B-42

Query Match      100.0%; Score 21; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YVAD 4
      |||||
Db      4 YVAD 7

RESULT 10
US-09-394-019B-43
; Sequence 43, Application US/09394019B
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
; FILE REFERENCE: 300-903820US
; CURRENT APPLICATION NUMBER: US/09/394,019B
; CURRENT FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide substrate
; NAME/KEY: MOD_RES
; LOCATION: (3)..(3)
; OTHER INFORMATION: X is Alb
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-394-019B-43

Query Match      100.0%; Score 21; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YVAD 4
      |||||
Db      4 YVAD 7

RESULT 11
US-09-394-019B-287
; Sequence 287, Application US/09394019B
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
; FILE REFERENCE: 300-903820US
; CURRENT APPLICATION NUMBER: US/09/394,019B
; CURRENT FILING DATE: 1999-09-10
```

```
; NAME/KEY: MOD_RES
; LOCATION: (3)..(3)
; OTHER INFORMATION: X is Alb
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-394-019B-42

Query Match      100.0%; Score 21; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YVAD 4
      |||||
Db      4 YVAD 7

RESULT 10
US-09-394-019B-43
; Sequence 43, Application US/09394019B
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
; FILE REFERENCE: 300-903820US
; CURRENT APPLICATION NUMBER: US/09/394,019B
; CURRENT FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide substrate
; NAME/KEY: MOD_RES
; LOCATION: (3)..(3)
; OTHER INFORMATION: X is Alb
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-394-019B-43

Query Match      100.0%; Score 21; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YVAD 4
      |||||
Db      4 YVAD 7

RESULT 11
US-09-394-019B-287
; Sequence 287, Application US/09394019B
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
; FILE REFERENCE: 300-903820US
; CURRENT APPLICATION NUMBER: US/09/394,019B
; CURRENT FILING DATE: 1999-09-10
```

```
; NAME/KEY: MOD_RES
; LOCATION: (3)..(3)
; OTHER INFORMATION: X is Alb
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-394-019B-42

Query Match      100.0%; Score 21; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YVAD 4
      |||||
Db      4 YVAD 7

RESULT 10
US-09-394-019B-43
; Sequence 43, Application US/09394019B
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
; FILE REFERENCE: 300-903820US
; CURRENT APPLICATION NUMBER: US/09/394,019B
; CURRENT FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide substrate
; NAME/KEY: MOD_RES
; LOCATION: (3)..(3)
; OTHER INFORMATION: X is Alb
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-394-019B-43

Query Match      100.0%; Score 21; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YVAD 4
      |||||
Db      4 YVAD 7

RESULT 11
US-09-394-019B-287
; Sequence 287, Application US/09394019B
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
; FILE REFERENCE: 300-903820US
; CURRENT APPLICATION NUMBER: US/09/394,019B
; CURRENT FILING DATE: 1999-09-10
```

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; NAME/KEY: MOD_RES
; LOCATION: (3)..(3)
; OTHER INFORMATION: X is Alb
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa is alpha-aminoisobutyric acid
US-09-394-019B-287

Query Match      100.0%; Score 21; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YVAD 4
      |||||
Db      4 YVAD 7

RESULT 12
US-09-394-019B-288
; Sequence 288, Application US/09394019B
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
; FILE REFERENCE: 300-903820US
; CURRENT APPLICATION NUMBER: US/09/394,019B
; CURRENT FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 288
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide. Chemically synthesized protease substrate.
; NAME/KEY: misc feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa is alpha-aminoisobutyric acid
US-09-394-019B-288

Query Match      100.0%; Score 21; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YVAD 4
      |||||
Db      4 YVAD 7

RESULT 13
US-09-394-019B-42
; Sequence 42, Application US/09394019B
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
```

```
/ TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
/ TITLE OF INVENTION: AND METHODS OF USE THEREOF
/ FILE REFERENCE: M-903820US
/ CURRENT APPLICATION NUMBER: US/09/394,019B
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: PCT/US98/00300
/ PRIOR FILING DATE: 1998-02-20
/ PRIOR APPLICATION NUMBER: US 08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ NUMBER OF SEQ ID NOS: 257
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 42
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (3)..(3)
/ OTHER INFORMATION: Xaa is Aib
/ US-09-394-019B-42

Query Match          100.0%; Score 21; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YVAD 4
        ||||
Db      4 YVAD 7

RESULT 14
US-09-394-019B-43
/ Sequence 43, Application US/09394019B
/ GENERAL INFORMATION:
/ APPLICANT: Oncoimmunin, Inc.
/ APPLICANT: Komoriya, Akira
/ APPLICANT: Packard, Beverly
/ TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
/ FILE REFERENCE: M-903820US
/ CURRENT APPLICATION NUMBER: US/09/394,019B
/ CURRENT FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: PCT/US98/00300
/ PRIOR FILING DATE: 1998-02-20
/ PRIOR APPLICATION NUMBER: US 08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ NUMBER OF SEQ ID NOS: 257
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 43
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (3)..(3)
/ OTHER INFORMATION: Xaa is Aib
/ US-09-394-019B-43

Query Match          100.0%; Score 21; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YVAD 4
        ||||
Db      4 YVAD 7

RESULT 15
US-09-394-019C-42
```

```
/ Sequence 42, Application US/09394019C
/ GENERAL INFORMATION:
/ APPLICANT: Oncoimmunin, Inc.
/ APPLICANT: Komoriya, Akira
/ APPLICANT: Packard, Beverly
/ TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
/ FILE REFERENCE: 300-303820US
/ CURRENT APPLICATION NUMBER: US/09/394,019C
/ CURRENT FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: PCT/US98/00300
/ PRIOR FILING DATE: 1998-02-20
/ PRIOR APPLICATION NUMBER: US 08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ NUMBER OF SEQ ID NOS: 405
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 42
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (3)..(3)
/ OTHER INFORMATION: X is Aib
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (3)..(3)
/ OTHER INFORMATION: Xaa can be any naturally occurring amino acid
/ US-09-394-019C-42

Query Match          100.0%; Score 21; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YVAD 4
        ||||
Db      4 YVAD 7

Search completed: May 24, 2004, 14:48:20
Job time : 13.5 secs
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 24, 2004, 14:36:18 ; Search time 13.5 Seconds
(without alignments)
28.501 Million cell updates/sec

Title: US-09-765-105A-1

Perfect score: 21

Sequence: 1 YVAD 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	32	2 S20719	alcohol dehydrogen
2	21	100.0	43	2 A24553	cuticle protein SC
3	21	100.0	54	2 H82718	hypothetical prote
4	21	100.0	66	2 PC4222	GTP-binding protei
5	21	100.0	66	2 PC4266	GTP-binding protei
6	21	100.0	68	2 G82969	probable transcrip
7	21	100.0	75	2 AC1251	hypothetical prote
8	21	100.0	76	2 S51629	FEAC-6 protein -
9	21	100.0	77	1 R3BS18	ribosomal protein
10	21	100.0	80	2 AG1613	hypothetical prote
11	21	100.0	82	2 IS1103	Major Histocompati
12	21	100.0	82	2 IS1106	Major Histocompati
13	21	100.0	82	2 E71321	hypothetical prote
14	21	100.0	86	2 A28093	GTP-binding protei
15	21	100.0	88	2 S71291	retrovirus-related
16	21	100.0	88	2 H87560	conserved hypotet
17	21	100.0	94	2 G69597	conserved hypotet
18	21	100.0	94	2 AB2197	hypothetical prote
19	21	100.0	95	2 A43027	T-cell receptor va
20	21	100.0	97	2 AD4409	glutathione transf
21	21	100.0	97	2 AD2153	hypothetical prote
22	21	100.0	98	2 F97952	phospho-beta-gluc
23	21	100.0	99	2 A87437	hypothetical prote
24	21	100.0	101	2 A47450	HNF-3/fork-head ho
25	21	100.0	102	2 T29100	hypothetical prote
26	21	100.0	102	2 B88860	conserved hypotet
27	21	100.0	106	2 D90247	conserved hypotet
28	21	100.0	112	2 C23766	modulation protein
29	21	100.0	113	2 D27664	T-cell receptor be

30 21 100.0 113 2 D64593 ferredoxin-like pr
31 21 100.0 113 2 F71919 chain of 2-oxogluc
32 21 100.0 113 2 D70757 probable regulator
33 21 100.0 114 2 G84409 hypothetical prote
34 21 100.0 115 2 H86734 HU-like DNA-bindin
35 21 100.0 119 2 D95146 conserved hypotet
36 21 100.0 119 2 C98014 conserved hypotet
37 21 100.0 120 2 AF0108 probable DNA bindi
38 21 100.0 120 2 ABC490 probable regulator
39 21 100.0 122 1 RWMSC5 T-cell receptor be
40 21 100.0 122 2 F84287 hypothetical prote
41 21 100.0 123 2 T49794 hypothetical prote
42 21 100.0 125 2 S01374 cuticle protein LC
43 21 100.0 129 2 S78097 endocuticular prot
44 21 100.0 130 2 AE1355 hypothetical prote
45 21 100.0 131 2 A99502 conserved hypotet

ALIGNMENTS

RESULT 1

S20719

alcohol dehydrogenase related protein (EC 1.1.1.1.) - fruit fly (*Drosophila yakuba*) (fr
N/Alternate names: Adh-dup protein; Adh-related protein; Adhr protein; alcohol dehydro
C/Species: *Drosophila yakuba*
C/Date: 20-Feb-1995 #sequence_revision 19-Apr-1996 #text_change 11-Jun-1999
C/Accession: S20719

R.Ashburner, M.
submitted to the EMBL Data Library, July 1990

A/Reference number: S20713

A/Accession: S20719

A/Molecule type: DNA

A/Residues: 1-32 <ASH>

A/Cross-references: EMBL:X54120; NID:g9214; PIDN:CAA38064.1; PID:g9216

C/Genetics:

A/Gens: FlyBase:Adhr; Adh-dup

A/Cross-references: FlyBase:FBgn0013164

C/Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

C/Keywords: Oxidoreductase

Query Match 100.0%; Score 21; DB 2; Length 32;

Best Local Similarity 100.0%; Pred. No. 54; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

QY 1 YVAD 4

DB 11 YVAD 14

RESULT 2

A24553

cuticle protein SC1 - flesh fly (*Sarcophaga bullata*) (fragment)

C/Species: *Sarcophaga bullata*

C/Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 18-Jun-1993

C/Accession: A24553

R/Henzel, W.J.; Mole, J.E.; Mulligan, K.; Lipke, H.

J. Mol. Evol. 22, 39-45, 1985

A/Title: *Sarcophagid* larval proteins: partial sequence homologies among three cuticle
A/Reference number: A32963; MUID:86037264; PMID:3932663

A/Accession: A24553

A/Molecule type: protein

A/Residues: 1-43 <HEN>

C/Superfamily: cuticle protein LCPI

Query Match 100.0%; Score 21; DB 2; Length 43;

Best Local Similarity 100.0%; Pred. No. 74; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

QY 1 YVAD 4

DB 39 YVAD 42

RESULT 3
 H82718
 hypothetical protein XP1129 [imported] - Xylella fastidiosa (strain 9a5c)
 C/Species: Xylella fastidiosa
 C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C/Accession: H82718
 R/Accession: H82718
 C/Comment: The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing
 Nature 406, 151-157, 2000
 A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A/Reference number: A82515; MUID:20365717; PMID:10910347
 A/Note: for a complete list of authors see reference number A59328 below
 A/Accession: H82718
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-54 <STM>
 A/Cross-references: GB:AE003949; GB:AE003849; NID:g9106088; PIDN:AAF83939.1; GSPDB:GN001
 A/Experimental source: strain 9a5c
 R/Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; B
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Canargo, L.E.A.; Carraro, D.M.; Carrier, H
 as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A/Authors: Ferreira, V.C.A.; Ferro, J.S.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
 A/Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.B.; de Sa, R.G.; Santelli, R.V.; Sawasak
 A/Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
 M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A/Reference number: A59328
 A/Contents: annotation
 C/Genetics:
 A/Gene: XF1129
 Query Match 100.0%; Score 21; DB 2; Length 54;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YVAD 4
 Db 50 YVAD 53

RESULT 4
 PC4222
 GTP-binding protein rhoA - pig (fragment)
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 20-Jun-2000
 C/Accession: PC4222
 R/Nishimura, J.; Sakihara, C.; Zhou, Y.; Kanaide, H.
 Biochem. Biophys. Res. Commun. 227, 750-754, 1996
 A/Title: Expression of rho A and rho kinase mRNAs in porcine vascular smooth muscle.
 A/Reference number: PC4222; MUID:97040692; PMID:8886005
 A/Accession: PC4222
 A/Molecule type: mRNA
 A/Residues: 1-66 <NIS>
 A/Cross-references: DDBJ:D89492; NID:g1695730; PIDN:BAAL1966.1; PID:g1695731
 C/Comment: This protein is involved in the inhibition of myosin light chain phosphatase.
 C/Genetics:
 A/Gene: rhoA
 C/Superfamily: ras transforming protein; translation elongation factor Tu homology
 C/Keywords: GTP binding
 Query Match 100.0%; Score 21; DB 2; Length 66;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YVAD 4
 Db 7 YVAD 10

RESULT 5
 PC4266
 GTP-binding protein rhoA - rat (fragment)
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 13-Aug-1999
 C/Accession: PC4266
 R/Niito, N.; Nishimura, J.; Sakihara, C.; Nakano, H.; Kanaide, H.
 Biochem. Biophys. Res. Commun. 230, 356-359, 1997
 A/Title: Up-regulation of rho A and rho-kinase mRNAs in the rat myometrium during pregn
 A/Reference number: PC4266; MUID:97168976; PMID:9016783
 A/Accession: PC4266
 A/Molecule type: mRNA
 A/Residues: 1-66 <NII>
 A/Comment: This protein is involved in the Ca2+ sensitivity of the smooth muscle myofil
 C/Superfamily: ras transforming protein; translation elongation factor Tu homology
 C/Keywords: GTP binding
 Query Match 100.0%; Score 21; DB 2; Length 66;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YVAD 4
 Db 7 YVAD 10

RESULT 6
 G82969
 probable transcription regulator PA5403 [imported] - Pseudomonas aeruginosa (strain PAO
 C/Species: Pseudomonas aeruginosa
 C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C/Accession: G82969
 R/Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
 Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A/Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic path
 A/Reference number: A82950; MUID:20437337; PMID:10984043
 A/Accession: G82969
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-68 <STO>
 A/Cross-references: GB:AE004953; GB:AE004091; NID:g9951727; PIDN:AAG08788.1; GSPDB:GN00
 A/Experimental source: strain PAO1
 C/Genetics:
 A/Gene: PA5403
 Query Match 100.0%; Score 21; DB 2; Length 68;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YVAD 4
 Db 64 YVAD 67

RESULT 7
 AC1251
 hypothetical protein lnc1411 [imported] - Listeria monocytogenes (strain EGD-e)
 C/Species: Listeria monocytogenes
 C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
 C/Accession: AC1251
 R/Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke
 ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H
 D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A/Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M
 ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland
 A/Title: Comparative genomics of Listeria species.
 A/Reference number: AB1077; MUID:21537279; PMID:11679669
 A/Accession: AC1251
 A/Status: preliminary
 A/Molecule type: DNA

A;Residues: 1-75 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAC99489.1; PID:gl6410840; GSPDB:GNO0177
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lnc1411

Query Match 100.0%; Score 21; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
DB 65 YVAD 68

RESULT 8
S51629
FRAC-6 protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 24-Sep-1999
C;Accession: S51629
R;Pierrou, S.; Hellqvist, M.; Samuelsson, L.; Enerbaeck, S.; Carlsson, P.
EMBO J. 13, 5002-5012, 1994
A;Title: Cloning and characterization of seven human forkhead proteins: binding site spe
A;Reference number: S51624; MUID:95045392; PMID:7957066
A;Accession: S51629
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-76 <PE>
A;Cross-references: EMBL:U13224; NID:g563167; PIDN:AAA92041.1; PID:g563168
C;Genetics:
A;Gene: GDB:FKHL10; FRAC6
A;Cross-references: GDB:450228; OMIM:601093
A;Map position: 5q34-q34
C;Superfamily: unassigned fork head DNA-binding domain homology
P;6-76/Domain: fork head DNA-binding domain homology (fragment) <FHD>

Query Match 100.0%; Score 21; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
DB 35 YVAD 38

RESULT 9
R3BS18
ribosomal protein S18 - Bacillus stearothermophilus
C;Species: Bacillus stearothermophilus
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 30-Jun-1993
C;Accession: S03556
R;McDougall, J.; Choli, T.; Kruff, V.; Kapp, U.; Wittmann-Liebold, B.
FEBS Lett. 245, 253-260, 1989
A;Title: The complete amino acid sequence of ribosomal protein S18 from the moderate the
A;Reference number: S03556; MUID:89171319; PMID:2647521
A;Accession: S03556
A;Molecule type: protein
A;Residues: 1-77 <MCD>
C;Superfamily: Escherichia coli ribosomal protein S18
C;Keywords: protein biosynthesis; ribosome

Query Match 100.0%; Score 21; DB 1; Length 77;
Best Local Similarity 100.0%; Pred. No. 1.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
DB 73 YVAD 76

RESULT 10
AG1613

hypothetical protein lin1448 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AG1613
R;Glaser, P.; Prangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeck
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl,
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkak, G.; Madueno, E.; Maitournam, A.;
Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Varquez-Boland, J.A.; Voss, H.; Wehlian
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AG1613
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-80 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC96679.1; PID:gl6413921; GSPDB:GNO0178
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin1448

Query Match 100.0%; Score 21; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
DB 70 YVAD 73

RESULT 11
IS1103
Major Histocompatibility Complex class IIB - ring-necked pheasant (fragment)
C;Species: Phasianus colchicus (ring-necked pheasant)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999
C;Accession: IS1103
R;Witzell, H.; von Schantz, T.; Zoorob, R.; Auftray, C.
Immunogenetics 39, 395-403, 1994
A;Title: Molecular characterization of three Mhc class II B haplotypes in the ring-nec
A;Reference number: IS1103; MUID:94245280; PMID:7910588
A;Accession: IS1103
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-82 <MIT>
A;Cross-references: EMBL:X75403; NID:g496920; PIDN:CAA53157.1; PID:g496921
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 100.0%; Score 21; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
DB 42 YVAD 45

RESULT 12
IS1106
Major Histocompatibility Complex class IIB - ring-necked pheasant (fragment)
C;Species: Phasianus colchicus (ring-necked pheasant)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999
C;Accession: IS1106
R;Witzell, H.; von Schantz, T.; Zoorob, R.; Auftray, C.
Immunogenetics 39, 395-403, 1994
A;Title: Molecular characterization of three Mhc class II B haplotypes in the ring-nec
A;Reference number: IS1103; MUID:94245280; PMID:7910588
A;Accession: IS1106
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-82 <MIT>
A;Cross-references: EMBL:X75406; NID:g496926; PIDN:CAA53160.1; PID:g496927
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology

```
Query Match      100.0%; Score 21; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
   ||||
Db 42 YVAD 45

RESULT 13
EY1321
hypothetical protein TP0467 - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
C:Accession: EY1321
R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin,
rson, J.; Khaliq, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; McDoe
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A>Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770; PMID:9665876
A:Accession: EY1321
A>Status: Preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-82 <COL>
A:Cross-references: GB:AE001223; GB:AE000520; NID:93322745; PIDN:AAC65458.1; PID:9332275
A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0467

Query Match      100.0%; Score 21; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
   ||||
Db 31 YVAD 34

RESULT 14
A28093
GTP-binding protein rhoB - bovine (fragments)
N:Alternate names: 20K GTP-binding protein rho; rhoB* protein; transforming protein rhoB
C:Species: Bos primigenius taurus (cattle)
C>Date: 26-Jan-1989 #sequence_revision 05-Apr-1995 #text_change 13-Aug-1999
C:Accession: A28093; B38324; E60050
R:Yamamoto, K.; Kondo, J.; Hishida, T.; Teranishi, Y.; Takai, Y.
J. Biol. Chem. 263, 9926-9932, 1988
A>Title: Purification and characterization of a GTP-binding protein with a molecular wei
A:Reference number: A28093; MUID:88257127; PMID:3133371
A:Accession: A28093
A:Molecule type: protein
A:Residues: 25-47;48-53 <YAM>
A:Experimental source: brain
R:Williamson, K.C.; Smith, L.A.; Moss, J.; Vaughan, M.
J. Biol. Chem. 265, 20807-20812, 1990
A>Title: Guanine nucleotide-dependent ADP-ribosylation of soluble rho catalyzed by Clostr
A:Reference number: A38324; MUID:91065876; PMID:2174426
A:Accession: B38324
A:Molecule type: protein
A:Residues: 1-43;48-53;69-71 <WIL>
A:Experimental source: brain
R:Hoshijima, M.; Kondo, J.; Kikuchi, A.; Yamamoto, K.; Takai, Y.
Brain Res. Mol. Brain Res. 7, 9-16, 1990
A>Title: Purification and characterization from bovine brain membranes of a GTP-binding
C1 - identification as the rhoA gene product.
A:Reference number: A60050; MUID:90135940; PMID:2153899
A:Accession: B60050
A:Molecule type: protein
A:Residues: 54-68;72-86 <HO2>
A:Experimental source: brain
C:Genetics:
A:Gene: rhoB
```

C:Superfamily: ras transforming protein; translation elongation factor Tu homology
C:Keywords: GTP binding; immediate-early protein; transforming protein
F:51-54/Region: GTP-binding NKXD motif

Query Match 100.0%; Score 21; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
 ||||
Db 15 YVAD 18

RESULT 15
S71291
retrovirus-related reverse transcriptase homolog (clone Rcat3) - Arabidopsis thaliana (C:Species: Arabidopsis thaliana (mouse-ear cress))
A:Variety: Strain Columbia
C>Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C:Accession: S71291
R:Brandes, A.; Heslop-Harrison, J.S.; Kamm, A.; Kubis, S.; Doudrick, R.L.; Schmidt, T.
submitted to the EMBL Data Library, January 1996
A:Description: Comparative analysis of the chromosomal and genomic organization of Ty1-
A:Reference number: S71291
A:Accession: S71291
A:Molecule type: DNA
A:Residues: 1-88 <BRA>
A:Cross-references: EMBL:268911; NID:g1171493; PIDN:CAA93146.1; PID:g1171494
C:Genetics:
A:Mobile element: retrotransposon copia-like Ty1
C:Superfamily: retrovirus-related polyprotein
C:Keywords: reverse transcriptase

Query Match 100.0%; Score 21; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
 ||||
Db 20 YVAD 23

Search completed: May 24, 2004, 14:41:39
Job time : 14.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 24, 2004, 14:36:17 ; Search time 10.5 Seconds
(without alignments)
19.836 Million cell updates/sec

Title: US-09-765-105a-1

Perfect score: 21

Sequence: 1 YVAD 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	32	ADHR_DROYA	P2487 drosophila
2	21	100.0	36	PAHO_RABIT	P41336 oryctolagus
3	21	100.0	37	ATPO_SOLTU	P80504 solanum tub
4	21	100.0	43	CUP1_SARBU	P14485 sarcophaga
5	21	100.0	74	RS18_CHLTE	Q8kam3 chlorobium
6	21	100.0	75	HP18_SHORE	P80882 rhodospira
7	21	100.0	77	RS18_BACST	P10806 bacillus st
8	21	100.0	82	Y467_TREPA	Q83480 treponema p
9	21	100.0	94	YQGV_BACSU	P54499 bacillus su
10	21	100.0	102	CPA1_CANPG	P81575 cancer pagu
11	21	100.0	104	LCPS_DROME	P32192 drosophila
12	21	100.0	105	CPA2_CANPG	P81576 cancer pagu
13	21	100.0	113	YJ50_YCTTU	Q10868 mycobacteri
14	21	100.0	117	GLRA_ACALA	P30970 mus musculu
15	21	100.0	122	TVBS_MOUSE	P04213 mus musculu
16	21	100.0	125	CUI4_MANSE	P13229 manduca sex
17	21	100.0	126	CLP2_DROMI	P91627 drosophila
18	21	100.0	138	CLP1_DROMI	P91627 drosophila
19	21	100.0	143	CUI7_BOMMO	Q02387 bombyx mori
20	21	100.0	152	ACPM_DROME	Q84519 drosophila
21	21	100.0	156	CUS5_ARADI	P80518 araneus dia
22	21	100.0	159	CUS7_ARADI	P80519 araneus dia
23	21	100.0	159	OBP_BOVIN	P07435 bos taurus
24	21	100.0	161	HS21_MAIZE	P24631 zea mays (m
25	21	100.0	163	DTD_NSIWA	Q91st7 neisseria m
26	21	100.0	171	Y041_NPVOP	Q10301 oryglia pseu
27	21	100.0	174	AROK_STAAW	Q99tv6 staphylococ
28	21	100.0	174	AROK_STAAW	Q8nwc8 staphylococ
29	21	100.0	174	CUS2_BOMMO	Q02388 bombyx mori
30	21	100.0	180	CYSH_RHIRT	Q33579 rhizobium t
31	21	100.0	182	AFT_PSPPK	Q88f33 pseudomonas
32	21	100.0	182	NODC_RHILT	P04678 rhizobium l
33	21	100.0	184	CUPP_DROME	P14484 drosophila

34 21 100.0 186 1 YQEK_BACSU P54456 bacillus su
35 21 100.0 192 1 CUPP_DROPS P16369 drosophila
36 21 100.0 192 1 RHO1_DROME P48148 drosophila
37 21 100.0 192 1 RHO1_CHEEL Q22038 caenorhabdi
38 21 100.0 192 1 RHO1_CHEEL Q22038 caenorhabdi
39 21 100.0 192 1 RHO1_CHEEL Q22038 caenorhabdi
40 21 100.0 192 1 RHO1_CHEEL Q22038 caenorhabdi
41 21 100.0 193 1 RHO1_CHEEL Q22038 caenorhabdi
42 21 100.0 193 1 RHO1_CHEEL Q22038 caenorhabdi
43 21 100.0 193 1 RHO1_CHEEL Q22038 caenorhabdi
44 21 100.0 194 1 RHO1_CHEEL Q22038 caenorhabdi
45 21 100.0 198 1 RHO1_CHEEL Q22038 caenorhabdi

ALIGNMENTS

RESULT 1

ADHR_DROYA
ID ADHR_DROYA STANDARD; PRT; 32 AA.
AC P28487;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Alcohol dehydrogenase related 31 kDa protein (Fragment).
GN ADHR.
OS Drosophila yakuba (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7245;
RN [1]
RP SEQUENCE FROM N.A.
RA Ashburner M.;
RL Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
(SDR) family.
CC
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CC
CC EMBL; X54120; CAA38064.1; -
CC PIR; S20719; S20719.
CC FlyBase; FBgn0013164; Dyak\Adhr.
CC InterPro; IPR002198; ADH_short.
CC PROSITE; PS00061; ADH_SHORT; PARTIAL.
KW Oxidoreductase.
FT NP_BIND 11 >32 NAD OR NADP (BY SIMILARITY).
FT NON_TER 32
SQ SEQUENCE 32 AA; 3412 MW; 9302949AFCBE7D4F CRC64;
Query Match 100.0%; Score 21; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2

PAHO_RABIT
ID PAHO_RABIT STANDARD; PRT; 36 AA.
AC P41336;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Pancreatic hormone (Pancreatic polypeptide) (pp).
YQ 1 YVAD 4
DB 11 YVAD 14

GN PPV.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pancreas;
 RX MEDLINE=94130533; PubMed=8299350;
 RA Marks N.J., Shaw C., Halton D.W., Curry W.J., Thim L.;
 RT "Rabbit pancreatic polypeptide";
 RL Comp. Biochem. Physiol. 106B:883-887(1993).
 CC -!- FUNCTION: Pancreatic hormone is synthesized in pancreatic islets
 CC of Langerhans and acts as a regulator of pancreatic and
 CC gastrointestinal functions.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the NPY family.
 DR HSSP: P01302; IBBB.
 DR InterPro: IPR001955; Pancreatic_hormn.
 DR Pfam: PF00159; hormones; 1.
 DR PRINTS: PR00278; PANCHORMONE.
 DR SMART: SM00309; PAH; 1.
 DR PROSITE: PS00265; PANCREATIC_HORMONE_1; 1.
 DR PROSITE: PS00276; PANCREATIC_HORMONE_2; 1.
 KW Hormone; Amidation; Pancreas.
 FT MOD RES 36
 SQ SEQUENCE 36 AA; 4197 MW; AL4450831A7759D CRC64;

Query Match 100.0%; Score 21; DB 1; Length 36;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
 ||||
 DB 20 YVAD 23

RESULT 3
 ID_ATPO SOLTU STANDARD; PRT; 37 AA.
 AC P80504;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ATP synthase delta chain, mitochondrial (EC 3.6.3.14) (Oligomycin
 DE sensitivity conferral protein) (OSCP) (Fragment).
 OS Soluman tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Tuber;
 RX MEDLINE=97077345; PubMed=8919912;
 RA Jansch L., Kruft V., Schmitz U.K., Braun H.P.;
 RT "New insights into the composition, molecular mass and stoichiometry
 RT of the protein complexes of plant mitochondria";
 RL Plant J. 9:357-368(1996).
 CC -!- FUNCTION: This protein seems to be part of the stalk that links
 CC CF(0) to CF(1). It either transmits conformational changes from
 CC CF(0) into CF(1) or is implicated in proton conduction.
 CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
 CC H(+)(Out).
 CC -!- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic
 CC core - and CF(0) - the membrane proton channel. CF(1) has five
 CC subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0)
 CC has three main subunits: a, b and c.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial.
 CC -!- SIMILARITY: Belongs to the ATPase delta chain family.
 DR InterPro: IPR000711; APPTynt_OSCP.
 DR PROSITE: PS00389; ATPASE_DELTA; PARTIAL.
 KW Hydroxylase; ATP synthesis; CF(1); Hydrogen ion transport;

KW Mitochondrion.
 FT NON_TER 37
 SQ SEQUENCE 37 AA; 4003 MW; 95FDAB14A298F4AF CRC64;
 Query Match 100.0%; Score 21; DB 1; Length 37;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
 ||||
 DB 8 YVAD 11

RESULT 4
 ID_CUPL1 SARBU STANDARD; PRT; 43 AA.
 AC P14485;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Larval cuticle protein SC1 (Fragment).
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Sarcophagidae; Sarcophaga.
 OX NCBI_TaxID=7385;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=86037264; PubMed=3932563;
 RA Henzel W.J., Mole J.E., Mulligan K., Lipke H.;
 RT "Sarcophagid larval proteins: partial sequence homologies among three
 RT cuticle proteins and related structures of drosophilids";
 RL J. Mol. Evol. 22:39-45(1985).
 CC -!- FUNCTION: Component of the cuticle of the larva of flesh fly.
 CC -!- SIMILARITY: Contains 1 cuticle consensus domain.
 DR PIR: A24553; A24553.
 DR InterPro: IPR000618; Insect cuticle.
 DR Pfam: PFC0379; Chitin bind 4; 1.
 DR PROSITE: PS00233; CUTICLE; PARTIAL.
 KW Structural protein; Cuticle.
 FT NON_TER 43
 SQ SEQUENCE 43 AA; 4556 MW; 6B3FD9A0B67E2210 CRC64;
 Query Match 100.0%; Score 21; DB 1; Length 43;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
 ||||
 DB 39 YVAD 42

RESULT 5
 ID_RS18_CHLTE STANDARD; PRT; 74 AA.
 AC Q8KAW3;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE 30S ribosomal protein S18.
 GN RPSR OR C72133;
 OS Chlorobium tepidum.
 OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
 OC Chlorobium.
 OX NCBI_TaxID=1097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TLS / ATCC 49652 / DSM 12025;
 RX MEDLINE=22103685; PubMed=12093901;
 RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
 RA Dodson R.J., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H.,
 RA Hickey B.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,
 RA Holt I., Unayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,

RA Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,
RA Vamachan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,
RA Venter J.C., Tettelin H., Bryant D.A., Fraser C.M., Ketchum K.A.,
RT "The complete genome sequence of *Chlorobium tepidum* TJS, a
RT photosynthetic, anaerobic, green-sulfur bacterium";
RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514 (2002).
CC -1- FUNCTION: Binds as a heterodimer with protein S6 to the central
CC domain of the 16S rRNA, where it helps stabilize the platform of
CC the 30S subunit (By similarity).
CC -1- SUBUNIT: Part of the 30S ribosomal subunit. Forms a tight
CC heterodimer with protein S6 (By similarity).
CC -1- SIMILARITY: Belongs to the S18P family of ribosomal proteins.
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DR EMBL; AE012962; AAM73349.1; --
DR TIGR; CT2133; --
DR HAMAP; MF 00270; -; 1.
DR InterPro; IPR001648; Ribosomal_S18.
DR Pfam; PF01084; Ribosomal_S18; 1.
DR PRINTS; PR00974; RIBOSOMALS18.
DR ProDom; PD002239; Ribosomal_S18; 1.
DR TIGRFAMs; TIGR00165; S18; 1.
DR ProDom; PD002239; Ribosomal_S18; 1.
DR PROSITE; PS00057; RIBOSOMAL_S18; FALSE NEG.
DR Ribosomal protein, RNA-binding; rRNA-binding; Complete proteome.
KW RIBOSOMAL PROTEIN; RNA-BINDING; rRNA-BINDING; Complete proteome.
SQ SEQUENCE 74 AA; 8671 MW; 71204A5284DE8B CRC84;

Query Match 100.0%; Score 21; DB 1; Length 74;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
| | | |
DB 68 YVAD 71

RESULT 6
ID HPIS_RHOPE STANDARD; PRT; 75 AA.
AC P08082;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE High potential iron-sulfur protein (HiPIP).
GN HIP.
OS Rhodospirillum rubrum.
CC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
CC Comamonadaceae; Rhodospirillum.
CC NCBI_TaxID=28066;
CC [1]
CC SEQUENCE
RC STRAIN=JMC 7819;
RX MEDLINE=97234565; PubMed=9119002;
RA van Briesche G., Clur S., Hochkoeppler A., van Beeumen J.J.;
RT "The primary structure of Rhodospirillum rubrum high-potential iron-
RT sulfur protein, an electron donor to the photosynthetic reaction
RT center";
RT Eur. J. Biochem. 244:371-377 (1997).
CC -1- FUNCTION: Specific class of high-redox-potential 4Fe-4S
CC ferredoxins. Functions in anaerobic electron transport in most
CC purple and in some other photosynthetic bacteria and in at least
CC one genus (Paracoccus) of halophilic, denitrifying bacteria.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- MASS SPECTROMETRY: MW=7849.64; METHOD=Electrospray.
CC -1- SIMILARITY: Belongs to the high potential iron-sulfur protein
CC (HiPIP) family.
CC HSP; P00260; 1CKU.

DR InterPro; IPR000170; Hipot_iron_sulf.
DR Pfam; PF01355; HiPIP; 1.
DR PROSITE; PS00596; HiPIP; 1.
KW Electron transport; Iron-sulfur; 4Fe-4S.
FT METAL 38 38 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 41 41 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 54 54 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 68 68 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ SEQUENCE 75 AA; 7849 MW; 9F6C8662A72D3 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 75;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
| | | |
DB 17 YVAD 20

RESULT 7
ID RS18_BACST STANDARD; PRT; 77 AA.
AC P10806;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 30S ribosomal protein S18 (BS21) (BS19).
GN RPSR.
OS Bacillus stearothermophilus.
CC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
CC NCBI_TaxID=1422;
CC [1]
CC SEQUENCE.
RC STRAIN=799;
RX MEDLINE=89171319; PubMed=2647521;
RA McDougall J., Choli T., Kruff V., Kapp U., Wittmann-Liebold B.;
RT "The complete amino acid sequence of ribosomal protein S18 from the
RT moderate thermophile *Bacillus stearothermophilus*.";
RL FEBS Lett. 245:253-260 (1989).
RN [2]
RP SEQUENCE OF 1-15.
RC STRAIN=10;
RX MEDLINE=75019590; PubMed=4607606;
RA Yaguchi M., Matheson A.T., Visentin L.P.;
RT "Prokaryotic ribosomal proteins: N-terminal sequence homologies and
RT structural correspondence of 30 S ribosomal proteins from *Escherichia*
RT coli and *Bacillus stearothermophilus*.";
RL FEBS Lett. 46:296-300 (1974).
CC -1- FUNCTION: Binds as a heterodimer with protein S6 to the central
CC domain of the 16S rRNA, where it helps stabilize the platform of
CC the 30S subunit (By similarity).
CC -1- SUBUNIT: Part of the 30S ribosomal subunit. Forms a tight
CC heterodimer with protein S6 (By similarity).
CC -1- SIMILARITY: Belongs to the S18P family of ribosomal proteins.
CC PIR; S03556; R3BS18.
DR HAMAP; MF 00270; -; 1.
DR InterPro; IPR001648; Ribosomal_S18.
DR Pfam; PF01084; Ribosomal_S18; 1.
DR PRINTS; PR00974; RIBOSOMALS18.
DR ProDom; PD002239; Ribosomal_S18; 1.
DR TIGRFAMs; TIGR00165; S18; 1.
DR PROSITE; PS00057; RIBOSOMAL_S18; 1.
KW Ribosomal protein; RNA-binding; rRNA-binding.
FT INIT MET 0
SQ SEQUENCE 77 AA; 8837 MW; A3F635FC64210E42 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 77;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
| | | |
DB 73 YVAD 76

Microbiology 142:3103-3111 (1996).

RL [2]
RN SEQUENCE FROM N.A.
RP STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., S.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Boriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
Entian K.D., Errington J., Fabret C., Ferrar E., Foulger D.,
Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleon N.,
Ghim S.Y., Glaser P., Goffeau A., Gligitsky E.J., Grandi G.,
Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudga B., Park S.H.,
Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
Srokcin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
"The complete genome sequence of the Gram-positive bacterium Bacillus subtilis".
RT Nature 390:249-256 (1997).
RL -!- SIMILARITY: BELONGS TO THE UPF0045 FAMILY.
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CC
CC
CC EMBL; D84432; BAA12525.1; -;
DR EMBL; Z99116; CAB14412.1; -;
DR PIR; G69957; G69957.
DR Subtilisin; BG11689; YGGV.
DR InterPro; IPR002787; DUF77.
DR Pfam; PF01910; DUF77; 1.
DR TIGRFAMs; TIGR00106; TIGR00106; 1.
DR Hypothetical protein; Complete proteome.
KW TIGRFAMs; TIGR00106; 1.
SQ SEQUENCE 94 AA; 10453 MW; 4A576F2338B80999 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 94;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
DB 21 YVAD 24
|||||

RESULT 10
CPAL CANFG STANDARD; PRT; 102 AA.
ID CPAL CANFG
AC P81575;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE Hypothetical protein YGGV.
GN YGGV OR BSU24810.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=168 / JH642;
RM MEDLINE=97124195; PubMed=6969508;
RA Mizuno M., Masuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,
Kobayashi Y.,
RT "Systematic sequencing of the 293 kb 210 degrees-232 degrees region of
RT the Bacillus subtilis genome containing the skin element and many
RT sporulation genes."
RT

OS Cancer pagurus (Rock crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubranchyura; Cancroidea; Cancridae; Cancer.
 OX NCBI_TaxID=6755;
 RN [1]
 RN SEQUENCE.
 RP TISSUE=Carapace cuticle;
 RC MEDLINE=99354472; PubMed=10425740;
 RX Andersen S.O.;
 RA "Exoskeletal proteins from the crab, *Cancer pagurus*.";
 RL Comp. Biochem. Physiol. 123A:203-211 (1999).
 CC -!- TISSUE SPECIFICITY: Arthrodiol membrane and calcified shell.
 CC -!- MASS SPECTROMETRY: MW=11139.8; METHOD=WALDI.
 CC -!- SIMILARITY: Contains 1 cuticle consensus domain.
 DR InterPro: IPR000618; Insect cuticle.
 DR Pfam: PF00379; Chitin bind_4; 1.
 DR PRINTS: PR00947; CUTICLE_FALSE_NEG.
 DR PROSITE: PS00233; CUTICLE; FALSE_NEG.
 KW Structural protein; Cuticle.
 SQ SEQUENCE 102 AA; 11142 MW; 17101253BF109533 CRC64;
 Query Match 100.0%; Score 21; DB 1; Length 102;
 Best Local Similarity 100.0%; Pred. No. 90;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YVAD 4
 DB 63 YVAD 66
 RESULT 11
 LCPS_DROME STANDARD; PRT; 104 AA.
 AC P92192; O96905;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Larval cuticle protein V precursor.
 GN (LCP65AB1 OR LCP5 OR DCP3-ALPHA OR CG18776) AND
 GN (LCP65AB2 OR LCP5 OR DCP3-BETA OR CG18773).
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Oregon-R;
 RA Mandalaparthi P., Jiang S., Schneider G., Chihara C.;
 RT "The cuticle proteins of *Drosophila melanogaster*: sequence of Lcp5 in
 RT the third chromosome cluster.";
 RN Dros. Info. Service 77:49-51 (1996).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Iso-1;
 RX MEDLINE=98043412; PubMed=9383064;
 RA Charles J.-P., Chihara C., Nejad S., Riddiford L.M.;
 RT "A cluster of cuticle genes of *Drosophila* at 65A: sequence, structure
 RT and evolution.";
 RL Genetics 147:1213-1224 (1997).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=107311132;
 RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA Anantides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
 RA George R.A., Lewis S.E., Yandell M.D., Zhang Q., Chen L.X.,
 RA Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-U., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foslter C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck C.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jastoli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laslo P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mervulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195 (2000).
 RN [4]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=22426066; PubMed=12537569;
 RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
 RA George R.A., Guarini H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
 RA Rubin G.M., Celniker S.E.;
 RT "A *Drosophila* full-length cDNA resource.";
 RN Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8 (2002).
 RN [5]
 RN SEQUENCE OF 19-32
 RC STRAIN=Oregon-R; TISSUE=Larva;
 RX MEDLINE=98318806; PubMed=9654737;
 RA Charles J.-P., Chihara C., Nejad S., Riddiford L.M.;
 RT "Identification of proteins and developmental expression of RNAs
 RT encoded by the 65A cuticle protein gene cluster in *Drosophila*
 RT melanogaster.";
 RL Insect Biochem. Mol. Biol. 28:131-138 (1998).
 CC -!- FUNCTION: Component of the cuticle of the larva.
 CC -!- SIMILARITY: Contains 1 cuticle consensus domain.
 CC -----
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 CC -----
 DR EMBL; U81550; AAB00301.1; -;
 DR EMBL; U84746; AAB88065.1; -;
 DR EMBL; U84747; AAB88066.1; -;
 DR EMBL; A5003563; AAG22328.1; -;
 DR EMBL; A5003563; AAG22331.1; -;
 DR EMBL; AY071366; AAL48988.1; -;
 DR FlyBase; FBgn0020644; Lcp65Ab1.
 DR FlyBase; FBgn0020643; Lcp65Ab2.
 DR InterPro: IPR000618; Insect cuticle.
 DR Pfam: PF00379; Chitin bind_4; 1
 DR PROSITE; PS00233; CUTICLE; FALSE_NEG.
 KW Structural protein; Cuticle; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 104 LARVAL CUTICLE PROTEIN V.

```

FT CONFLICT 62 72 AAVVHGSFTWV -> CRCEPRILHLG (IN REF. 1).
SQ SEQUENCE 104 AA; 11267 MW; BA60DD9483DD6992 CRC64;

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 104;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
DB 84 YVAD 87

RESULT 12
CPA2 CANPG STANDARD; PRT; 105 AA.
AC P81576;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cuticle protein AML159 (CPAM1159).
OS Cancer pagurus (Rock crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubranchyura; Cancroidea; Cancridae; Cancer.
OX NCBI_TaxID=6755;
RN [1]
RP SEQUENCE.
RC TISSUE=Carapace cuticle;
RX MEDLINE=93354472; PubMed=10425740;
RA Andersen S.O.;
RT "Exoskeletal proteins from the crab, Cancer pagurus.";
RL Comp. Biochem. Physiol. 123A:203-211(1999).
CC -I- TISSUE SPECIFICITY: Arthropod membrane.
CC -I- MASS SPECTROMETRY: MW=11582.8; METHOD=MALDI.
CC -I- SIMILARITY: Contains 1 cuticle consensus domain.
DR InterPro; IPR00618; Insect cuticle.
DR Pfam; PF00379; Chitin bind_4; 1.
DR PRINTS; PR00947; CUTICLE.
DR PROSITE; PS00233; CUTICLE; 1.
DR Structural protein; Cuticle.
KW Structural protein; Cuticle.
SQ SEQUENCE 105 AA; 11586 MW; 6C8827FA4E149729 CRC64;

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 105;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
DB 63 YVAD 66

RESULT 13
YJ90 MYCTU STANDARD; PRT; 113 AA.
AC Q10868;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein RV1990C/MT2044/MB2012c precursor.
GN RV1990C OR MT2044 OR WTCV39.29 OR MB2012C.
OS Mycobacterium tuberculosis, and
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773, 1765;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=H37Rv;
RX MEDLINE=9829598; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

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RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulton J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL J. Bacteriol. 184:5479-5490(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=M.bovis; STRAIN=AF2122/97;
RX MEDLINE=22709107; PubMed=12789972;
RA Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duthoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RT "The complete genome sequence of Mycobacterium bovis.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
RN [4]
RP SEQUENCE FROM N.A.
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RN [5]
RP SEQUENCE FROM N.A.
RC ENBL; Z74025; CA98394.1; -.
DR ENBL; AE007056; AAK46320.1; -.
DR ENBL; BX248341; CAD96865.1; -.
DR PIR; D70757; D70757.
DR TIGR; MT2044; -.
DR Tuberculist; RV1990c; -.
DR Hypothetical protein; Signal; Complete proteome.
FT SIGNAL 1 13 POTENTIAL.
FT CHAIN 14 113 HYPOTHETICAL PROTEIN
PT RV1990C/MT2044/MB2012C.
SQ SEQUENCE 113 AA; 12488 MW; 41978D1BE45874C9 CRC64;

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 113;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
DB 58 YVAD 61

RESULT 14
GLHA ACALA STANDARD; PRT; 117 AA.
AC P30970;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Glycoprotein hormones alpha chain precursor (Gonadotropin alpha
DE chain) (GTH-alpha).
OS Acanthopagrus latus (Yellowfin porgy).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Acanthopagrus.

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OX NCBI_TaxID=8177;
RN [1]
RP SEQUENCE FROM N.A.
RA Tsai H.J., Chen Y.L.;
RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in gametogenesis and steroidogenesis.
CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the glycoprotein hormones alpha chain
CC family.
CC
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CC -----
DR HSP; P01215; 1XUL.
DR HSP; P01215; 1XUL.
DR InterPro: IPR002400; GF_CysKnot.
DR InterPro: IPR000476; Glyco_hormone.
DR Pfam: PF00236; hormone6; 1.
DR PRINTS: PRO0438; GFCYSKNOT.
DR PRINTS: PRO0274; GLYCOHORMONE.
DR ProDom: PD002047; Glyco_hormone; 1.
DR SMART: SM00067; GH; 1.
DR PROSITE: PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR PROSITE: PS00780; GLYCO_HORMONE_ALPHA_2; 1.
DR PROSITE: PS00277; GLYCO_HORMONE_ALPHA_3; 1.
KW Hormone; Glycoprotein; Signal.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 117 GLYCOPROTEIN HORMONES ALPHA CHAIN.
FT DISULFID 34 57 BY SIMILARITY.
FT DISULFID 37 86 BY SIMILARITY.
FT DISULFID 54 107 BY SIMILARITY.
FT DISULFID 58 109 BY SIMILARITY.
FT DISULFID 55 112 BY SIMILARITY.
FT CARBOHYD 78 78 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 103 103 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 117 AA; 13061 MW; F9ACE213DB67AF14 CRC64;
Query Match 100.0%; Score 21; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YVAD 4
DB 19 YVAD 22
RESULT 15
TVB5_MOUSE
ID TVB5_MOUSE STANDARD; PRT; 122 AA.
AC F04213;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE T-cell receptor beta chain V region C5 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8503636; PubMed=6092964;
RA Fatten P., Yokota T., Rothbard J., Chien Y., Arai K., Davis M.M.;
RT "Structure, expression and divergence of T-cell receptor beta-chain
RT variable regions."
RL Nature 312:40-46(1984).
CC -!- MISCELLANEOUS: This sequence was derived from a T-helper clone.
DR PIR; A02008; RMSCS.
```

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DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW T-cell; Receptor; Immunoglobulin domain; Signal.
FT NON_TER 1 1
FT SIGNAL <1 7
FT CHAIN 8 122 T-CELL RECEPTOR BETA CHAIN V REGION C5.
FT DOMAIN 8 103 V SEGMENT.
FT DOMAIN 104 108 D SEGMENT.
FT DOMAIN 109 122 J SEGMENT.
FT DISULFID 31 99 BY SIMILARITY.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13349 MW; D657DCC9B261C64C CRC64;
Query Match 100.0%; Score 21; DB 1; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YVAD 4
DB 58 YVAD 61
Search completed: May 24, 2004, 14:39:33
Job time : 11.5 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 24, 2004, 14:36:17 ; Search time 36.5 Seconds
(without alignments)
34.577 Million cell updates/sec

Title: US-09-765-105A-1
Perfect score: 21
Sequence: 1 YVAD 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL.25.*

- 1: sp_arChaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	21	100.0	32	Q868A6	Q868A6 drosophila
2	21	100.0	44	11 Q8BJM4	Q8BJM4 mus musculus
3	21	100.0	45	9 Q858A7	Q858A7 mycobacteri
4	21	100.0	51	7 Q7VP64	Q7VP64 aethia cris
5	21	100.0	52	7 Q31335	Q31335 alligator m
6	21	100.0	52	7 Q31337	Q31337 alligator m
7	21	100.0	53	7 Q8SNE1	Q8SNE1 gallinago m
8	21	100.0	54	16 Q9PE99	Q9PE99 xylella fas
9	21	100.0	62	16 Q8Y145	Q8Y145 ralstonia s
10	21	100.0	62	16 Q8XSA4	Q8XSA4 ralstonia s
11	21	100.0	65	16 Q89DP2	Q89DP2 bradyrhizob
12	21	100.0	66	2 Q85X3	Q85X3 streptococ
13	21	100.0	66	6 F73275	F73275 sus scrofa
14	21	100.0	66	7 Q8SP36	Q8SP36 pygoscelsis
15	21	100.0	66	7 Q8SP52	Q8SP52 pygoscelsis
16	21	100.0	66	7 Q8SP50	Q8SP50 pygoscelsis

17	21	100.0	66	7 Q8SP33	Q8SP33 eudypsula m
18	21	100.0	66	7 Q8SP34	Q8SP34 eudypsula m
19	21	100.0	66	7 Q8SP51	Q8SP51 pygoscelsis
20	21	100.0	66	7 Q8SP40	Q8SP40 pygoscelsis
21	21	100.0	66	7 Q8SP37	Q8SP37 pygoscelsis
22	21	100.0	66	7 Q8SP43	Q8SP43 pygoscelsis
23	21	100.0	66	7 Q8SP38	Q8SP38 pygoscelsis
24	21	100.0	66	7 Q8SP32	Q8SP32 eudypsula m
25	21	100.0	66	7 Q8SP31	Q8SP31 eudypsula m
26	21	100.0	66	7 Q8SP35	Q8SP35 pygoscelsis
27	21	100.0	66	7 Q8SP48	Q8SP48 pygoscelsis
28	21	100.0	66	7 Q8SP42	Q8SP42 pygoscelsis
29	21	100.0	66	7 Q8SP45	Q8SP45 pygoscelsis
30	21	100.0	66	7 Q8SP41	Q8SP41 pygoscelsis
31	21	100.0	66	7 Q8SP39	Q8SP39 pygoscelsis
32	21	100.0	68	16 Q9HTG1	Q9HTG1 pseudomonas
33	21	100.0	68	16 Q88WV7	Q88WV7 lactobacill
34	21	100.0	69	16 Q8G3Y0	Q8G3Y0 bifidobacte
35	21	100.0	74	2 Q93RA0	Q93RA0 hydrog noba
36	21	100.0	75	2 Q9F428	Q9F428 listeria mo
37	21	100.0	75	16 Q8V784	Q8V784 listeria mo
38	21	100.0	76	16 Q8EKV5	Q8EKV5 oceanobacil
39	21	100.0	77	7 Q9TPP9	Q9TPP9 gallus gall
40	21	100.0	77	7 Q9TPP8	Q9TPP8 gallus gall
41	21	100.0	77	15 Q9Q706	Q9Q706 human immun
42	21	100.0	78	2 Q8VMK4	Q8VMK4 pseudomonas
43	21	100.0	78	16 Q88IL9	Q88IL9 pseudomonas
44	21	100.0	80	15 Q9WIS0	Q9WIS0 human immun
45	21	100.0	80	15 Q905E6	Q905E6 human immun

ALIGNMENTS

RESULT 1
Q868A6 PRELIMINARY; PRT; 32 AA.
ID Q868A6
AC Q868A6;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Alcohol dehydrogenase related protein (Fragment).
GN ADHR.
OS Drosophila miranda (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7229;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=0101.3, 0101.4, 0101.5, 0101.7, 0101.9, MA32, MA28, SPI38,
RC SP235, SP295, MSH22, and MSH38;
RA Yi S., Bachtrog D., Charlesworth B.;
RT "A survey of chromosomal and nucleotide sequence variation in
Drosophila miranda";
RL Genetics 0:0-0(2003);
DR EMBL; AY238770; AAO84926.1; -
DR EMBL; AY238771; AAO84928.1; -
DR EMBL; AY238772; AAO84930.1; -
DR EMBL; AY238773; AAO84932.1; -
DR EMBL; AY238774; AAO84934.1; -
DR EMBL; AY238775; AAO84936.1; -
DR EMBL; AY238776; AAO84938.1; -
DR EMBL; AY238777; AAO84940.1; -
DR EMBL; AY238778; AAO84942.1; -
DR EMBL; AY238779; AAO84944.1; -
DR EMBL; AY238780; AAO84946.1; -
DR EMBL; AY238781; AAO84948.1; -
FT NON TER 32
SQ SEQUENCE 32 AA; 3446 MW; 0F0D949AFCBE63BE CRC64;
Query Match 100.0%; Score 21; DB 5; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
11 YVAD 14

Db

RESULT 2

Q8BJM4 PRELIMINARY; PRT; 44 AA.

AC Q8BJM4; 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Protein kinase C-like 2 (Fragment).

GN 6030436C20RIK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Body;

RE MEDLINE=22354683; PubMed=12466851;

RA The FANTOM Consortium,

RA the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs";

RL Nature 420:563-573 (2002).

DR EMBL; AK062921; BAC38889.1; -

DR MGD; MGI:1925929; 6030436C20RIK.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

DR InterPro; IPR000961; Pkinase_C.

DR Pfam; PF00433; Pkinase_C; 1.

FT NON_TER 1

SQ SEQUENCE 44 AA; 5277 MW; FF86B72F23FF8AB2 CRC64;

Query Match 100.0%; Score 21; DB 11; Length 44;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
39 YVAD 42

Db

RESULT 3

Q858A7 PRELIMINARY; PRT; 45 AA.

AC Q858A7; 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Gp4.

OS Mycobacteriophage GJW1.

OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.

OX NCBI_TaxID=205869;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=22592660; PubMed=12705866;

RA Pedulla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadsworth C., Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pannunzio N.R., Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S., Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W., Hatfull G.F.;

RT "Origins of highly mosaic mycobacteriophage genomes.";

RL EMBL 113:171-182 (2003).

DR EMBL; AY129331; AAN01619.1; -

SQ SEQUENCE 45 AA; 5310 MW; DDE073829E591F73 CRC64;

Query Match 100.0%; Score 21; DB 9; Length 45;

Best Local Similarity 100.0%; Pred. No. 2.8e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
6 YVAD 9

Db

RESULT 4

Q7YP64 PRELIMINARY; PRT; 51 AA.

AC Q7YP64; 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE MHC class II antigen B (Fragment).

OS Aethia cristatella (Crested auklet).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Charadriiformes; Alcidae; Aethia.

OX NCBI_TaxID=28685;

RN [1]

RP SEQUENCE FROM N.A.

RC Walsh H.E., Friesen V.L.;

RT "A comparison of intra-specific patterns of DNA sequence variation in mitochondrial DNA, a-enolase, and MHC class II B loci in Auklets (Charadriiformes: Alcidae).";

RT Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

RL EMBL; AY327429; AAP93579.1; -

DR NON_TER 1

FT NON_TER 51

SQ SEQUENCE 51 AA; 5834 MW; 51AD1C39EF56C3EC CRC64;

Query Match 100.0%; Score 21; DB 7; Length 51;

Best Local Similarity 100.0%; Pred. No. 3.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
4 YVAD 7

Db

RESULT 5

Q31335 PRELIMINARY; PRT; 52 AA.

AC Q31335; 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE MHC class II B protein (Fragment).

GN MHC CLASS II B.

OS Alligator mississippiensis (American alligator).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Crocodylidae; Alligatorinae; Alligator.

OX NCBI_TaxID=8496;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=American alligator; TISSUE=Blood;

RX MEDLINE=96137171; PubMed=8564010;

RA Edwards S.V., Grann M., Potts W.K.;

RT "Dynamics of Mhc evolution in birds and crocodilians: amplification of class II genes with degenerate primers.";

RL MGI. Scol. 4:719-729 (1995).

DR EMBL; U24402; AAA99113.1; -

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0045012; F:MHC class II receptor activity; IEA.

DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.

DR GO; GO:0019886; P:antigen processing, exogenous antigen via M. . .; IEA.

DR GO; GO:0006955; P:immune response; IEA.

DR InterPro; IPR000353; MHC_II_beta.

DR Pfam; PF00969; MHC_II_beta; 1.

DR ProDom; PD000328; MHC_II_beta; 1.

DR Glycoprotein; MHC II; Transmembrane.

FT NON_TER 1

```

FT NON_TER 52 52
SQ SEQUENCE 52 AA; 6198 MW; D5405DA025C11698 CRC64;

Query Match 100.0%; Score 21; DB 7; Length 52;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
DB 24 YVAD 27

RESULT 6
Q31337
ID Q31337 PRELIMINARY; PRT; 52 AA.
AC Q31337;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE MHC class II B protein (Fragment).
DE MHC CLASS II B.
GN Alligator mississippiensis (American alligator).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX NCBI_TaxID=8496;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=American alligator; TISSUE=Blood;
RX MEDLINE=9613771; PubMed=8564010;
RA Edwards S.V., Grahm M., Potts W.K.;
RT "Dynamics of Mhc evolution in birds and crocodilians: amplification of
class II genes with degenerate primers.";
RL Mol. Ecol. 4:719-729(1995).
DR EMBL; U24404; AAA9115.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0045012; F: MHC class II receptor activity; IEA.
DR GO; GO:0019884; P: antigen presentation, exogenous antigen; IEA.
DR GO; GO:0019886; P: antigen processing, exogenous antigen via M. . .; IEA.
DR GO; GO:0006955; P: immune response; IEA.
DR InterPro; IPR000353; MHC II beta.
DR Pfam; PF00969; MHC II beta.
DR ProDom; PD000328; MHC II beta.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1 1
FT NON_TER 52 52
SQ SEQUENCE 52 AA; 6199 MW; D84EBDA025C11698 CRC64;

Query Match 100.0%; Score 21; DB 7; Length 52;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
DB 24 YVAD 27

RESULT 7
Q8SNE1
ID Q8SNE1 PRELIMINARY; PRT; 53 AA.
AC Q8SNE1;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE MHC class II antigen B (Fragment).
DE MHC class II antigen B (Fragment).
OS Gallinago media (great snipe).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Charadriiformes; Scolopacidae;
OC Gallinago.
OX NCBI_TaxID=114734;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=gall 6;
RX Ekblom R., Grahm M., Hoglund J.;
RA
```

```

RT "Patterns of polymorphism in the MHC class II of a non-passerine bird,
the great snipe (Gallinago media).";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF485412; AAL93175.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0045012; F: MHC class II receptor activity; IEA.
DR GO; GO:0019884; P: antigen presentation, exogenous antigen; IEA.
DR GO; GO:0019886; P: antigen processing, exogenous antigen via M. . .; IEA.
DR GO; GO:0006955; P: immune response; IEA.
DR InterPro; IPR000353; MHC II beta.
DR Pfam; PF00969; MHC II beta.
DR ProDom; PD000328; MHC II beta.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1 1
FT NON_TER 53 53
SQ SEQUENCE 53 AA; 6235 MW; F8A0B0E3C316727 CRC64;

Query Match 100.0%; Score 21; DB 7; Length 53;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
DB 26 YVAD 29

RESULT 8
Q9PE99
ID Q9PE99 PRELIMINARY; PRT; 54 AA.
AC Q9PE99;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Hypothetical protein Xf1129.
GN Xf1129.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9a5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.N., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Wenzek C.P.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhari A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuchioka M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR EMBL; AE003949; AAF83939.1; -.
DR FIR; H82718; H82718.
```

RT "Penicillin-binding protein 2b of *Streptococcus pneumoniae* in
RT piperacillin-resistant laboratory mutants."; J. Bacteriol. 176:5574-5577(1994).

DR GO; GO:0008658; F:penicillin binding; IEA.
 DR GO; GO:0009273; P:cell wall biosynthesis (sensu Bacteria); IEA.
 DR InterPro; IPR001460; Transpeptidase.
 DR Pfam; PF00905; Transpeptidase; 1.
 FT NON_TER 1 66
 FT NON_TER 66
 SQ SEQUENCE 66 AA; 7089 MW; 673DA1BCEC74B980 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 66;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
 DB 8 YVAD 11

RESULT 13
 P79275 PRELIMINARY; PRT; 66 AA.
 AC P79275;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Rho A (Fragment).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=domestic; TISSUE=Pulmonary vein;
 RX MEDLINE=97040692; PubMed=8986005;
 RA Nishimura J., Sakinaka C., Zhou Y., Kanaide H.;
 RT "Expression of Rho A and Rho-kinase mRNAs in Porcine Vascular Smooth
 Muscle.";
 RL Biochem. Biophys. Res. Commun. 227:750-754 (1996).
 DR EMBL; D89492; BAAL3966.1; -.
 DR PIR; PC4222; PC4222.
 DR HSSP; P06749; 1FTN.
 DR GO; GO:0008525; F:GTP binding; IEA.
 DR GO; GO:0003925; F:small monomeric GTPase activity; IEA.
 DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
 DR InterPro; IPR001806; Ras_transfrmg.
 DR Pfam; PF00071; ras; 1.
 KW GTP-binding.
 FT NON_TER 1 1
 FT NON_TER 66
 SQ SEQUENCE 66 AA; 7562 MW; 38C71B220AD67C30 CRC64;

Query Match 100.0%; Score 21; DB 6; Length 66;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
 DB 7 YVAD 10

RESULT 14
 Q8SP36 PRELIMINARY; PRT; 66 AA.
 AC Q8SP36;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE MHC class II antigen (Fragment).
 GN PYPA1.10.
 OS Pygoscelis papua (Gentoo penguin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Sphenisciformes; Spheniscidae;
 OC Pygoscelis.
 OX NCBI_TaxID=30457;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21655119; PubMed=11797106;
 RA Tsuda T.T., Tsuda M., Naruse T., Kawata H., Ando A., Shiina T.,
 RA Fukuda M., Kurita M., Lemaho I., Kulski J.K., Inoko H.;
 RT "Phylogenetic analysis of penguin(Spheniscidae) species based on
 RT sequence variation in MHC class II genes.";
 RL Immunogenetics 53:712-716(2001).
 DR EMBL; AB043599; BAB86830.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0045012; F:MHC class II receptor activity; IEA.
 DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.
 DR GO; GO:0019886; P:antigen processing, exogenous antigen; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR000353; MHC_II_beta.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 66
 SQ SEQUENCE 66 AA; 7774 MW; A955F9736710EADF CRC64;

Query Match 100.0%; Score 21; DB 7; Length 66;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
 DB 29 YVAD 32

RESULT 15
 Q8SP52 PRELIMINARY; PRT; 66 AA.
 AC Q8SP52;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Major histocompatibility complex (Fragment).
 GN PYAN1.01.
 OS Pygoscelis antarctica (Chinstrap penguin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Sphenisciformes; Spheniscidae;
 OC Pygoscelis.
 OX NCBI_TaxID=79643;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21655119; PubMed=11797106;
 RA Tsuda T.T., Tsuda M., Naruse T., Kawata H., Ando A., Shiina T.,
 RA Fukuda M., Kurita M., Lemaho I., Kulski J.K., Inoko H.;
 RT "Phylogenetic analysis of penguin(Spheniscidae) species based on
 RT sequence variation in MHC class II genes.";
 RL Immunogenetics 53:712-716(2001).
 DR EMBL; AB043556; BAB86820.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0045012; F:MHC class II receptor activity; IEA.
 DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.
 DR GO; GO:0019886; P:antigen processing, exogenous antigen; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR000353; MHC_II_beta.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 66
 SQ SEQUENCE 66 AA; 7839 MW; 841AD0C80029FDC7 CRC64;

Query Match 100.0%; Score 21; DB 7; Length 66;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
 DB 29 YVAD 32

Db 29 YVAD 32

Search completed: May 24, 2004, 14:41:00
Job time : 38.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 24, 2004, 14:36:17 ; Search time 51 Seconds
(without alignments)
22.161 Million cell updates/sec

Title: US-09-765-105A-2

Perfect score: 21

Sequence: 1 DEVD 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	4	2	AAW06250 ICE pepti
2	21	100.0	4	2	AAW76200 Mouse cas
3	21	100.0	4	2	AAW52756 Aminometh
4	21	100.0	4	2	AAW48940 Apopain (
5	21	100.0	4	2	AAW56305 Peptide c
6	21	100.0	4	2	AAW48948 Apopain (
7	21	100.0	4	2	AAW15622 Peptide u
8	21	100.0	4	2	AAW04114 Enzyme co
9	21	100.0	4	2	AAW68554 Apopain a
10	21	100.0	4	2	AAW24411 Caspase p
11	21	100.0	4	2	AAW99676 Caspase r
12	21	100.0	4	2	AAW94093 Protease
13	21	100.0	4	3	AAW78347 Caspase 1
14	21	100.0	4	3	AAW69646 Caspase i
15	21	100.0	4	3	AAW99958 Tetrapopt
16	21	100.0	4	3	AAW22889 Caspase-3
17	21	100.0	4	3	AAW49940 Synthetic
18	21	100.0	4	3	AAW79040 Caspase 1
19	21	100.0	4	3	AAW88373 Peptide u
20	21	100.0	4	3	AAW83396 DEVD pept
21	21	100.0	4	3	AAW68511 Synthetic
22	21	100.0	4	3	AAW80786 Fluoropho
23	21	100.0	4	3	AAW17431 Caspase 3
24	21	100.0	4	3	AAW69866 PARP clea
25	21	100.0	4	3	AAW10870 Aminocoum

ALIGNMENTS

RESULT 1

AAWC6250

ID AAW06250 standard; peptide; 4 AA.

XX AC AAW06250;

DT 03-MAR-1997 (first entry)

DE ICE peptide substrate.

XX Mch2; Ced-3/Ice; cysteine protease; apoptosis; autoimmune disease;

XX cancer; HIV; Alzheimer's disease; therapy.

OS Synthetic.

XX WO9636698-A1.

XX 21-NOV-1996.

XX 16-MAY-1996; 96WO-US007010.

XX 18-MAY-1995; 95US-00446925.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Litwack G, Alnemri ES, Fernandez-Alnemri T;

XX WFI; 1997-012077/01.

XX New isolated apoptotic cysteine protease, Mch 2 - used to develop prods. for use as anti-apoptotic agents or as cytotoxic agents.

XX Disclosure; Page 28; 43pp; English.

XX A tetrapeptide (AAW06250) represents a site present in poly (ADP- ribose) that is cleaved by an interleukin-1 beta converting enzyme (ICE)-like protein during apoptosis. Another tetrapeptide (AAW06453) is the ICE cleavage site in pro-interleukin-1 beta. The 2 peptides were used to test the activity of human Cpp32, ICE and 2 isoforms, alpha (see also AAW06244) and beta (AAW06245), of novel human apoptotic cysteine protease Mch2. Enzymatic activities were studied in total bacterial extracts from cells expressing these enzymes as GST fusion proteins. Neither Mch2 alpha nor Mch2 beta was able to cleave the YVAD substrate. Mch2 alpha, but not Mch2 beta, cleaved the DEVD substrate, but was 150-fold less active than Cpp32

XX Sequence 4 AA;

SQ

AAW67491 Caspase 3
AAW81937 APF agonist
AAW57561 Synthetic
AAW87641 Caspase 3
AAW26704 Caspase s
AAW81392 Caspase s
AAW21110 Synthetic
AAW56897 Caspase i
AAW79591 Caspase-3
AAW28540 Caspase-3
AAW21941 Control p
AAW32120 Tetrapept
AAW59582 Chromogen
AAW11216 Caspase-3
AAW62552 Cresyl vi
AAW62560 Cresyl vi
AAW62557 Cresyl vi
AAW62546 Cresyl vi
AAW67377 Peptide s
AAW67378 Peptide s

26 21 100.0 4 3 AAW67491
27 21 100.0 4 3 AAW81937
28 21 100.0 4 3 AAW57561
29 21 100.0 4 3 AAW87641
30 21 100.0 4 3 AAW26704
31 21 100.0 4 3 AAW81392
32 21 100.0 4 3 AAW21110
33 21 100.0 4 3 AAW56897
34 21 100.0 4 3 AAW79591
35 21 100.0 4 3 AAW28540
36 21 100.0 4 3 AAW21941
37 21 100.0 4 3 AAW32120
38 21 100.0 4 3 AAW59582
39 21 100.0 4 3 AAW11216
40 21 100.0 4 3 AAW62552
41 21 100.0 4 3 AAW62560
42 21 100.0 4 3 AAW62557
43 21 100.0 4 3 AAW62546
44 21 100.0 4 3 AAW67377
45 21 100.0 4 3 AAW67378

Query Match 100.0%; Score 21; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
 ||||
 Db 1 DEVD 4

RESULT 2
 AAW76200
 ID AAW76200 standard; protein; 4 AA.
 AC AAW76200;
 XX
 XX 26-NOV-1998 (first entry)
 DT
 XX Mouse caspase I peptide motif #2.
 DE
 XX Caspase; thymocyte; inhibitor; immature; treatment; cancer; autoreactive;
 KW leukaemia; melanoma; autoimmune disease; apoptosis; lymphocyte; T cell;
 KW receptor; infection; inflammatory disease; neurodegenerative disorder.
 XX
 OS Mus sp.
 XX
 XX WO9836057-A1.
 FN
 XX 20-AUG-1998.
 PD
 XX 17-FEB-1998; 98WO-US03524.
 PF
 XX 18-FEB-1997; 97US-00802474.
 PR 09-OCT-1997; 97US-00948124.
 XX
 XX (DAND) DANA FARBER CANCER INST INC.
 PA (PROC-) PROCEPT INC.
 XX
 PI Reinherz E, Clayton L, Ocain TD, Patch RJ;
 XX
 XX WPI; 1998-520756/44.
 DR
 XX Identifying agents which inhibit or enhance caspase activity - and which
 PT may be used, e.g., in treatment of cancer or autoimmune diseases.
 XX
 XX Disclosure; Page 8; 62pp; English.
 PS
 XX AAW76198-W76202 are peptides used in a method for identifying an agent
 CC which inhibits a caspase expressed in immature thymocytes. Such agents
 CC may be used in the treatment of cancers (such as leukaemia or melanomas)
 CC and autoimmune diseases. Inhibition of apoptosis can result in the
 CC inhibition of lymphocyte down regulation, resulting in a T cell receptor
 CC population with an increased proportion of autoreactive T cells, i.e., an
 CC increased occurrence of T cells which have specificity for the host
 CC animal's own cells (e.g. cancer cells). By the same token, increasing the
 CC activity of the caspase enzyme enhances apoptosis of self-recognising T
 CC cells, resulting in a decrease in the population of T cells which are
 CC responsible for autoimmune disorders. The compounds may also be useful in
 CC treating infections, inflammatory diseases and neurodegenerative
 CC disorders
 XX
 XX Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
 ||||
 Db 1 DEVD 4

RESULT 3
 AAW52756

AAWS2756 standard; peptide; 4 AA.
 AAW52756;
 XX
 XX 02-MAR-1999 (first entry)
 DT
 XX Aminomethylcoumarin-substituted tetrapeptide.
 DE
 XX Aminomethylcoumarin; fluorescent; interleukin; ICE; caspase;
 KW positional scanning synthetic combinatorial library.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Modified-site 1 /note= "the N-terminal is acetylated"
 FT Modified-site 4
 FT /note= "the C-terminal is condensed onto 7-amino- 4-
 FT methyl-coumarin via an amide linkage"
 XX
 XX GB2324529-A.
 PN
 XX 28-OCT-1998.
 PD
 XX 20-FEB-1998; 98GB-00003559.
 PF
 XX 21-FEB-1997; 97US-0038656P.
 PR
 XX (MERI) MERCK & CO INC.
 PA
 XX Chapman KT, Nicholson D, Rano T, Thornberry N;
 PI
 XX WPI; 1998-523841/45.
 DR
 XX New tetrapeptide coumarin derivatives - useful in combinatorial libraries
 PT to identify substrate specificity of cysteine or serine proteases e.g.
 PT interleukin-1 converting enzyme.
 XX
 XX Claim 3; Page 42; 49pp; English.
 PS
 XX The peptide is a specifically claimed example of new aminomethyl-
 CC coumarin-labelled tetrapeptides of formula Ac-Xaa-Xaa-Xaa-asp-AMC. The
 CC tetrapeptides are used to generate a fluorescent positional scanning
 CC synthetic combinatorial library for the investigation of the substrate
 CC specificity of cysteine and serine proteases, e.g. in the analysis of
 CC interleukin-1 beta converting enzyme substrates and other caspase
 CC substrates, and to identify inhibitors which may mediate inflammations.
 CC The library preferably comprises a mixture of at least 200 of the
 CC tetrapeptides
 XX
 XX Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
 ||||
 Db 1 DEVD 4

RESULT 4
 AAW48940
 ID AAW48940 standard; protein; 4 AA.
 AC AAW48940;
 XX
 XX 26-OCT-1998 (first entry)
 DT
 XX Apopain (caspase-3) peptide substrate.
 DE
 XX Apopain; caspase-3; protease; SPA; tyrosine phosphatase;
 KW scintillation proximity binding assay; diabetes; cancer;

KW 4-phosphono(difluoromethyl) phenylalanine group; osteoporosis.
 OS Synthetic.
 XX
 XX JP10099075-A.
 XX
 XX 21-APR-1998.
 PD
 XX
 XX Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl."
 FT Modified-site 4
 FT Modified-site 4 /note= "Optional attachment to aldehydes or ketones"
 FT
 XX
 XX WO9820024-A1.
 PN
 XX
 XX 14-MAY-1998.
 PD
 XX
 XX 03-NOV-1997; 97WO-CA000824.
 PF
 XX
 XX 04-NOV-1996; 96US-0030411P.
 PR
 XX
 XX (MERI) MERCK PROSST CANADA INC.
 PA
 XX
 XX Desmarais S, Friesen R, Zamboni R;
 PI
 XX
 XX WPI; 1998-348101/30.
 DR
 XX
 XX Peptide(s) useful in binding assays for tyrosine phosphatases or cysteine
 PT proteases - contain two or more 4-phosphono(difluoromethyl) phenylalanine
 PT groups to improve binding affinity.
 PT
 XX
 XX Example; Page 29; 59pp; English.
 PS
 XX
 XX Variants of the apopain (caspase-3) peptide substrate can be used as
 CC ligands for the binding assay used in the invention. The invention
 CC provides a method for use in a scintillation proximity binding assay
 CC (SPA) for proteases and phosphatases. The method involves using mutated
 CC proteases and phosphatases whereby the catalytic cysteine residue of the
 CC enzymes are replaced with a serine or alanine residue to correct the
 CC problem of interference in SPA from extraneous oxidizing and alkylating
 CC agents. The mutation affects the catalytic properties of the enzyme but
 CC does not affect their binding properties. The invention claims for new
 CC ligands for use in SPA which have increased binding affinity for a
 CC tyrosine phosphatase or cysteine protease. The ligands contain at least
 CC two 4-phosphono(difluoromethyl) phenylalanine groups which increase
 CC binding affinity of the ligand to its respective enzyme. The assay can be
 CC used to determine the ability of new ligands and compound mixtures to
 CC competitively bind with an enzyme. The method is claimed to allow a
 CC better usage of SPA in the discovery of compounds for the treatment and
 CC study of diseases, e.g. diabetes, cancer and osteoporosis
 CC
 XX
 SQ Sequence 4 AA;
 Query Match 100.0%; Score 21; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DEVD 4
 Db ||||
 1 DEVD 4
 RESULT 5
 AAW56305 standard; peptide; 4 AA.
 ID AAW56305
 XX
 XX AAW56305;
 AC
 XX
 XX 22-JUL-1998 (first entry)
 DT
 XX
 XX Peptide cleaved by interleukin-1-beta-converting enzyme-like protein.
 DE
 XX
 XX N-acetyl-DEVD-methyl coumarinamide; MCA;
 KW interleukin-1- beta converting enzyme-like activity; ICE activity;
 KW cysteine protease; investigation; substrate specificity.
 XX

OS Synthetic.
 XX
 XX JP10099075-A.
 PN
 XX
 XX 21-APR-1998.
 PD
 XX
 XX 30-SEP-1996; 96JP-00276813.
 PF
 XX
 XX 30-SEP-1996; 96JP-00276813.
 PR
 XX
 XX (SHIS) SHISEIDO CO LTD.
 PA
 XX
 XX WPI; 1998-289868/26.
 DR
 XX
 XX Protein with interleukin-1-beta converting enzyme-like activity - useful
 PT in investigation of substrate specificity in, e.g. Parkinson's disease.
 PT
 XX
 XX Disclosure; Page 2; 5pp; Japanese.
 PS
 XX
 XX The present sequence, N-acetyl-DEVD-methyl coumarinamide (MCA),
 CC represents a sequence that is cleaved by a protein with interleukin-1-
 CC beta converting enzyme (ICE)-like activity. The protein, which is
 CC obtained from human keratinocytes, has a relative molecular weight of 80
 CC kDa. The ICE protein is part of the cysteine protease family and is
 CC useful for investigation of the mechanism of substrate specificity (e.g.
 CC Alzheimer's disease, Parkinson's disease, autoimmune disease, lymphoma,
 CC cancer and apoptosis)
 CC
 XX
 XX Sequence 4 AA;
 Query Match 100.0%; Score 21; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DEVD 4
 Db ||||
 1 DEVD 4
 RESULT 6
 AAW48948 standard; protein; 4 AA.
 ID AAW48948
 XX
 XX AAW48948;
 AC
 XX
 XX 26-OCT-1998 (first entry)
 DT
 XX
 XX Apopain (caspase-3) peptide substrate.
 DE
 XX
 XX Apopain; caspase-3; protease; SPA; tyrosine phosphatase;
 KW scintillation proximity binding assay; diabetes; cancer;
 KW 4-phosphono(difluoromethyl) phenylalanine group; osteoporosis.
 XX
 XX Synthetic.
 OS
 XX
 XX Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 4
 FT Modified-site 4 /note= "Optional attachment to aldehydes or ketones"
 FT
 XX
 XX WO9820156-A1.
 PN
 XX
 XX 14-MAY-1998.
 PD
 XX
 XX 03-NOV-1997; 97WO-CA000825.
 PF
 XX
 XX 04-NOV-1996; 96US-0030408P.
 PR
 XX
 XX (MERI) MERCK PROSST CANADA INC.
 PA
 XX
 XX Desmarais S, Friesen R, Gresser M, Kennedy B, Nicholson D;
 PI Ramachandran C, Skorey K, Ford-Hutchinson A;

XX WPI; 1998-348103/30.
 XX Enzyme binding assay for detection of useful compounds - uses mutant form
 PT of wild-type enzyme, in which serine replaces cysteine at active site, to
 PT reduce interference from oxidising/alkylating agents.
 XX Example; Page 28; 63pp; English.
 XX Variants of the apocain (caspase-3) peptide substrate can be used as
 CC ligands for the binding assay used in the invention. The invention claims
 CC for a method for use in a scintillation proximity binding assay (SPA) for
 CC proteases and phosphatases. The method involves using mutated proteases
 CC and phosphatases whereby the catalytic cysteine residue of the enzymes
 CC are replaced with a serine or alanine residue to correct the problem of
 CC interference in SPA from extraneous oxidising and alkylating agents. The
 CC mutation affects the catalytic properties of the enzyme but does not
 CC affect their binding properties. The invention provides new ligands for
 CC use in SPA which have increased binding affinity for a tyrosine
 CC phosphatase or cysteine protease. The ligands contain at least two 4-
 CC phosphono(difluoromethyl) phenylalanine groups which increase binding
 CC affinity of the ligand to its respective enzyme. The assay can be used to
 CC determine the ability of new ligands and compound mixtures to
 CC competitively bind with an enzyme. The method is claimed to allow a
 CC better usage of SPA in the discovery of compounds for the treatment and
 CC study of diseases, e.g. diabetes, cancer and osteoporosis
 XX SQ Sequence 4 AA;
 XX Query Match 100.0%; Score 21; DB 2; Length 4;
 XX Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DEVD 4
 DB ||||
 1 DEVD 4
 RESULT 7
 AAY15622
 ID AAY15622 standard; peptide; 4 AA.
 AC AAY15622;
 XX 27-JUL-1999 (first entry)
 DT Peptide used to make fluorescent reporter molecules.
 DE Fluorogenic; fluorescent reporter molecule; enzyme substrate; apoptosis;
 KW protease; peptidase; apoptosis cascade; cancer; chemotherapeutic agent;
 KW cell death; viral protease activity.
 XX Synthetic.
 OS WO9918856-A1.
 XX 22-APR-1999.
 PD 09-OCT-1998; 98WO-US021231.
 PF 10-OCT-1997; 97US-0061582P.
 PR 03-MAR-1998; 98US-00033661.
 XX (CYTO-) CYTOVIA INC.
 PA Weber E, Cai SX, Keana JFW, Drewe JA, Zhang H;
 XX WPI; 1999-312448/26.
 XX New fluorogenic or fluorescent reporter molecules.
 XX Claim 3; Page 160; 202pp; English.

CC AAY15618-Y15759 represent peptides used to make the fluorogenic or
 CC fluorescent reporter molecules of the invention. These molecules contain
 CC a peptide moiety (e.g. present sequence) which acts as a substrate for
 CC enzymes involved in apoptosis or protease or peptidase enzymes. The
 CC compounds can be used as fluorogenic or fluorescent substrates for
 CC enzymes. Depending on the peptide moiety used, the fluorescent molecules
 CC can be used for detecting or measuring the activity of an enzyme involved
 CC in the apoptosis cascade in cells; to determine whether a test compound
 CC has an effect on an enzyme involved in the apoptosis cascade in cells;
 CC for determining the sensitivity of an animal with cancer to treatment
 CC with chemotherapeutic agents or determining whether a test substance
 CC inhibits, prevents, causes or enhances cell death of test cells; for
 CC detecting or measuring the activity of a viral protease in cells; for
 CC determining whether a test compound has an effect on the activity of a
 CC viral protease in cells; and for measuring the activity or determining
 CC whether a test substance has an effect on the activity of a protease or
 CC peptidase in cells
 XX SQ Sequence 4 AA;
 XX Query Match 100.0%; Score 21; DB 2; Length 4;
 XX Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DEVD 4
 DB ||||
 1 DEVD 4
 RESULT 8
 AAY04114
 ID AAY04114 standard; peptide; 4 AA.
 XX AAY04114;
 AC AAY04114;
 XX 15-JUN-1999 (first entry)
 DT Enzyme component #2 caspase recognition sequence.
 DE Cross-linked polypeptide assay; cross-linked enzyme component; cleavage;
 KW HIV; protease cleavage site.
 KW Synthetic.
 OS WO9906537-A1.
 XX 11-FEB-1999.
 PD 23-JUL-1998; 98WO-US015343.
 PF 30-JUL-1997; 97US-00302766.
 PR (BOE) BOEHRINGER MANNHEIM CORP.
 PA Powell MJ, Khanna P, Eisenbeis SJ, Lingenfelter D, Tietze LF;
 XX Manning W;
 PI WPI; 1999-190002/16.
 DR New cross-linked enzyme components - which have inhibited ability to
 XX complement with other enzyme components to form an active enzyme complex.
 PT Example 10; Page 34; 56pp; English.
 CC The present invention describes a cross-linked enzyme component (A),
 CC which: (i) has an inserted enzyme recognition site (ERS) in a polypeptide
 CC of the component; and (ii) has at least one covalent intrachain cross-
 CC link between amino acid side chains of the polypeptide. The component
 CC forms an enzymatically active complex with a second enzyme component,
 CC upon cleavage of the ERS, but is inhibited from forming this complex,
 CC prior to cleavage. The complex has enzymatic activity which is different
 CC from that of beta-galactosidase. The component may be used for
 CC measurement of substances in biological samples. It is especially useful

CC for measurement of enzymes (e.g. proteases, particularly viral,
 CC phosphatases, glycosidase, amidase and esterase) in clinical samples, or
 CC for measurement of target polynucleotides. Assay methods using the new
 CC components exhibit extremely low inherent background signals, due to
 CC reduction or inhibition of complementation of enzyme components prior to
 CC cleavage. The present sequence represents a peptide from an example of
 CC the present invention

XX Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
 DB 1 DEVD 4

RESULT 9
 AAW68554
 ID AAW68554 standard; protein; 4 AA.

XX AC AAW68554;
 XX DT 25-JAN-1999 (first entry)
 XX DE Apopain aldehyde-inhibitor peptide L-761191.
 XX KW Inhibitor; apopain; binding site; crystal structure; primer; PCR;
 XX KW amplification; Escherichia coli; apoptosis.
 XX OS Synthetic.

XX Key Location/Qualifiers
 FT Modified-site 1
 FT Modified-site 4 /notes= "acylated N-terminus"
 FT Modified-site 4 /notes= "contains C-terminal aldehyde group replacing
 FT Modified-site 4 carboxyl group"

PN US5834228-A.
 XX 10-NOV-1998.

XX 13-FEB-1997; 97US-00800007.

XX 13-FEB-1997; 97US-00800007.

XX (MERI) MERCK & CO INC.

XX (MERI) MERCK FROSST CANADA INC.

XX Thornberry NA, Gallant M, Fazil KM, Nicholson DW, Peterson EP;
 PI Rasper DM, Labelle M, Vaillancourt JP, Rotonda J, Ruel R, Becker JW;
 PI Gareau Y;

DR WPI; 1999-008706/01.

XX Identifying inhibitors of apopain by rational drug design - from ability
 PT to bind to the enzyme's substrate binding domain, potentially useful for
 PT inhibiting apoptosis, e.g. in treatment of acquired immune deficiency
 PT syndrome, autoimmune disease, infections etc.

XX Claim 1; Col 29; 22pp; English.

XX The invention relates to the identification of inhibitors of apopain by
 CC designing and synthesising a potential inhibitor that will form non-
 CC covalent bonds with amino acids in the apopain substrate binding site
 CC based upon the crystal structure co-ordinates of an apopain:acetyl-DEVD-
 CC CHO complex, testing it for apopain inhibition. Production of apopain for
 CC the binding studies comprises expression of the p17 and p12 subunits
 CC separately. This sequence represents an aldehyde-inhibitor of apopain
 CC designated L-761191. The apopain inhibitors are potentially useful for

CC inhibiting apoptosis
 XX Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
 DB 1 DEVD 4

RESULT 10
 AAY24411
 ID AAY24411 standard; peptide; 4 AA.

XX AC AAY24411;
 XX DT 20-SEP-1999 (first entry)
 XX DE Caspase processing site peptide #2 in aldehyde form.
 XX KW Human; caspase; anti-apoptosis; processing site; aldehyde; apoptosis;
 XX KW hepatitis; ischaemic cerebral disease; Alzheimer's disease; cancer;
 XX KW diarrhoea; bone marrow toxicity.

XX OS Homo sapiens.
 XX OS Synthetic.

XX PN JP11180891-A.

XX PD 06-JUL-1999.

XX PF 25-DEC-1997; 97JP-00356757.

XX PR 25-DEC-1997; 97JP-00356757.

XX PA (DAUC) DAIICHI PHARM CO LTD.

XX DR WPI; 1999-439401/37.

XX New anti-apoptosis agents - useful for treating hepatitis, ischemic
 PT cerebral diseases and Alzheimer's disease.

XX Claim 6; Page 6; 7pp; Japanese.

XX The present invention describes anti-apoptosis agent(s) containing human
 CC caspase and/or inhibitor(s) of its inducer(s), (especially human caspase-
 CC 1, human caspase-3 and/or a human caspase-3 inducer) comprising de-
 CC processing the process of human caspase inhibitor into active type of
 CC human caspase inducer. Also describes are anti-apoptosis agent(s)
 CC containing a modified protein comprising amino acid sequence around the
 CC processing site of caspase, especially aldehyde form of protein composed
 CC of amino acids of Tyr-Val-Ala-Asp, Asp-Glu-Val-Asp, and Glu-Ser-Met-Asp,
 CC especially Glu-Ser-Met-Asp, used for treatment of disease caused by
 CC apoptosis including hepatitis, ischaemic cerebral diseases, Alzheimer's
 CC disease, adverse reactions of bone marrow toxicity and diarrhoea due to
 CC administration of anticancer agent, especially hepatitis. The agent(s)
 CC are useful for treating disease caused by apoptosis e.g. ischaemic
 CC cerebral diseases, Alzheimer's disease, adverse reactions of bone marrow
 CC toxicity and diarrhoea due to administration of anticancer agent,
 CC especially hepatitis

XX Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
 DB 1 DEVD 4

RESULT 11
AAW99676
ID AAW99676 standard; peptide; 4 AA.
XX AC
XX AC AAW99676;
XX 03-JUN-1999 (first entry)
XX DT
XX DE Caspase recognition sequence.
XX DE
XX HIV; human immunodeficiency virus; cyclised prodrug; inhibition;
XX covalently cross-linked; cleavable site; suppression; inflammatory;
XX immunological activity; growth; cytotoxic effect.
XX OS Synthetic.
XX FN W09906072-A1.
XX PD 11-FEB-1999.
XX PF 24-JUL-1998; 98WO-US015433.
XX PR 30-JUL-1997; 97US-0054285P.
XX (BOE) BOEHRINGER MANNHEIM CORP.
XX FA Powell MJ;
XX FI WPI; 1999-167010/14.
XX DR
XX New polypeptide prodrugs - include, e.g. an inserted enzyme recognition
XX site and a covalent intrachain cross-link between amino acid side chains
XX of the polypeptide.
XX Example 10; Page 29; 44pp; English.
XX The present invention describes: (A) cross-linked prodrug, which: (i) has
XX an inserted enzyme recognition site (ERS) in a polypeptide of the prodrug
XX ; and (ii) has at least one covalent intrachain cross-link between amino
XX acid side chains of the polypeptide. The prodrug is converted to a
XX therapeutically more effective form upon cleavage of the ERS. (B) cross-
XX linked prodrug, which: (i) has an inserted ERS in a polypeptide of the
XX prodrug; and (ii) has at least one cross-linking moiety (CLM) covalently
XX bonded between amino acid side chains of the polypeptide. The CLM
XX comprises an enzymatically cleavable site. The prodrug is converted to a
XX therapeutically more effective form upon cleavage of this site. The
XX activated form of the prodrug may have any desired biological activity,
XX including activity in suppression of inflammatory or immunological
XX activity, promotion of growth or a direct cytotoxic effect on target
XX cells. Following cleavage of the ERS, the prodrug reassembles internally
XX by unfolding or refolding, or reassembles with one or more other
XX components, to form the therapeutic drug. In the activated form, the
XX prodrugs are at least 10 times more effective than the prodrug. The
XX present sequence represents a peptide used in an example from the present
XX invention
SQ Sequence 4 AA;
Query Match 100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DEVD 4
Db 1 DEVD 4
RESULT 12
AAW94093
ID AAW94093 standard; peptide; 4 AA.
XX AC

AAW94093;
XX 22-APR-1999 (first entry)
XX DE Protease inhibitor z-DEVD.FMK.
XX KW ICE; ALS; SOD gene; interleukin-1 converting enzyme; mutant; cell death;
XX anyotrophic lateral sclerosis; transgenic; ICE-like caspase; apoptosis;
XX traumatic brain injury; TBI; neurological; neurodegenerative; kidney;
XX heart disease; immune system; intestinal; aging; viral infection; AIDS;
XX acquired immune deficiency syndrome; gene therapy; protease inhibitor.
XX OS Synthetic.
XX Homo sapiens.
XX Key Location/Qualifiers
FT Modified-site 1 /note= "N-benzoyloxycarbonyl group is attached to Asp"
FT Modified-site 4
FT FT /note= "a fluoromethylketone (FMK) group is attached to
FT Asp"
XX W09857664-A1.
XX 23-DEC-1998.
XX 18-JUN-1998; 98WO-US012716.
XX 19-JUN-1997; 97US-0050242P.
XX (YUAN/) YUAN J.
XX (FRIE/) FRIEDLANDER R M.
XX Yuan J, Friedlander RM;
XX WPI; 1999-095294/08.
XX Treating anyotrophic lateral sclerosis (ALS) or ALS-like symptoms -
XX comprises inhibiting interleukin-1 converting enzyme (ICE) by gene
XX therapy, useful for treating central nervous system damage.
XX Example 8; Page 72; 96pp; English.
XX The invention relates to methods of treating anyotrophic lateral
XX sclerosis (ALS) or ALS-like symptoms that comprises inhibiting
XX interleukin-1 converting enzyme (ICE) by gene therapy. A mutant ICE gene
XX product can also be used for modulating programmed cell death
XX accompanying ALS. Transgenic non-human animal (including progeny)
XX containing a mutant ICE and SOD (ALS phenotype) gene are used to screen
XX compounds for treating ALS. Inhibitors of an ICE-like caspase are used to
XX attenuate or prevent apoptosis resulting from traumatic brain injury
XX (TBI), and to reduce the formation of reactive oxygen species following
XX TBI. Diseases caused by acute and chronic dysregulation of cell death,
XX which are treated by the ICE gene product, include malignant and pre-
XX malignant conditions, neurological, neurodegenerative disorders, heart
XX disease, immune system disorders, intestinal disorders, kidney disease,
XX aging, viral infections and acquired immune deficiency syndrome (AIDS).
XX The methods, mutant genes and inhibitors of ICE enable a better
XX understanding of the role of cell death and what triggers cell death in
XX ALS, which allow treatment of the disease. They also enable understanding
XX of the pathways mediating post traumatic apoptosis, which lead to novel
XX pharmacotherapy of TBI. Sequences AAW94092-94 represent protease
XX inhibitors (that can block effects of ICE gene product) for treating
XX patients with ALS symptoms
SQ Sequence 4 AA;
Query Match 100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DEVD 4
Db 1 DEVD 4

Db 1 DEVD 4

RESULT 13
 AAY78347
 ID AAY78347 standard; peptide; 4 AA.
 XX
 AC AAY78347;
 XX
 DT 05-MAY-2000 (first entry)
 XX
 DE Caspase 1 peptide Dns-SS-DEVD-CHO.
 XX
 KW Caspase; protein array; screening; biomolecular activity; proteomic;
 KW drug development; biosensor; diagnosis.
 XX
 OS Unidentified.
 XX
 PH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "Asp is N-terminally modified to dansyl-SS-Asp"
 FT Modified-site 4
 FT /note= "Asp is C-terminally modified to Asp-CHO"
 XX
 PN WO200004382-A1.
 XX
 XX 27-JAN-2000.
 PD
 XX 14-JUL-1999; 99WO-US015971.
 PF
 XX 14-JUL-1998; 98US-00115455.
 PR
 XX (ZYOM-) ZYOMYX INC.
 PA
 XX Wagner P, Ault-Riche D, Nock S, Itin C;
 PI
 XX WPI; 2000-171289/15.
 DR
 XX New arrays for analyzing components of a fluid sample, useful for drug
 PT development, functional proteomics, clinical diagnostics and biosensors.
 FT
 XX Example 7; Page 55; 81pp; English.
 PS
 XX The present invention describes an array (I) of proteins comprising a
 CC substrate, at least one organic thinfilm on some or all of the substrate
 CC surface, and patches arranged in discrete, known regions on portions of
 CC the substrate surface covered by organic thinfilm. Each of the patches
 CC comprises a protein immobilised on the underlying organic thinfilm. The
 CC arrays can be used for screening proteins for their ability to interact
 CC with a component of a sample. They can also be used for assaying for
 CC protein-protein binding interactions or analytes. They can be used for
 CC drug development, proteomics, clinical diagnostics and biosensors. The
 CC present sequence represents a peptide used in the exemplification of the
 CC present invention
 XX
 SQ Sequence 4 AA;
 Query Match 100.0%; Score 21; DB 3; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DEVD 4
 DB 1 DEVD 4
 RESULT 14
 AAY69646
 ID AAY69646 standard; peptide; 4 AA.
 XX
 AC AAY69646;
 XX
 DT 08-MAY-2000 (first entry)

XX Caspase inhibitor peptide #1.
 DE
 XX
 KW Caspase inhibitor; nitrogen-containing bisphosphonate; apoptosis;
 KW bone resorption; gastro-intestinal adverse effect; osteoporosis;
 KW Paget's disease; bone fracture; osteomalacia; periodontal disease;
 KW osteolysis.
 XX
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "Conjugated to a benzyloxycarbonyl (Z) N-terminal
 FT blocking group"
 FT Modified-site 4
 FT /note= "Conjugated to a fluoromethyl keto (FMK) C-
 FT terminal blocking group"
 XX
 PN WO9966945-A1.
 XX
 XX 29-DEC-1999.
 PD
 XX 21-JUN-1999; 99WO-US013961.
 PF
 XX 24-JUN-1998; 98US-0090497P.
 PR
 XX 15-JUL-1998; 98US-0092917P.
 PR
 XX 06-AUG-1998; 98GB-00017170.
 PR
 XX 02-SEP-1998; 98GB-00019126.
 PR
 XX (MERI) MERCK & CO INC.
 PA
 XX Reszka AA;
 PI
 XX WPI; 2000-147177/13.
 DR
 XX Composition containing nitrogen-containing bisphosphonate and caspase
 PT inhibitor, for inhibiting bone resorption, especially treatment of
 PT osteoporosis.
 PT
 XX Claim 5; Page 22; 33pp; English.
 PS
 XX Sequences AAY69646-Y69647 represent caspase inhibitor peptides which may
 CC be used in a novel composition for the inhibition of bone resorption. The
 CC composition comprises a nitrogen-containing bisphosphonate, or its salt,
 CC and a caspase inhibitor (such as peptides AAY69646-Y69647). Bone
 CC resorption may also be inhibited by sequential administration of a
 CC nitrogen-containing bisphosphonate and a caspase inhibitor. The nitrogen-
 CC containing bisphosphonate inhibits bone resorption by triggering
 CC apoptosis of osteoclasts. Although the caspase inhibitor has no effect on
 CC this process, it does inhibit a similar apoptotic action of the
 CC bisphosphonate on epithelial cells in the gastro-intestinal tract. The
 CC bisphosphonate/caspase inhibitor composition is used to inhibit bone
 CC resorption in mammals, specifically for oral treatment of osteoporosis
 CC (of any aetiology) and Paget's disease, but also in cases of
 CC osteomalacia, periodontal disease, periprosthetic osteolysis and bone
 CC fractures. The caspase inhibitor mitigates the adverse gastro-intestinal
 CC effects (e.g., oesophageal ulcers or oesophagitis), sometimes associated
 CC with oral administration of the bisphosphonate, resulting in safer
 CC treatment and better patient compliance
 XX
 SQ Sequence 4 AA;
 Query Match 100.0%; Score 21; DB 3; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DEVD 4
 DB 1 DEVD 4
 RESULT 15
 AAY9958

ID AAY99958 standard; peptide; 4 AA.
 AC AAY99958;
 XX
 DT 27-OCT-2000 (first entry)
 XX
 DE Tetrapeptide aldehyde which is a potent inhibitor of caspase-3.
 XX
 KW Inhibitor; apoptosis; cardiac; cerebral ischemia; stroke;
 KW type I diabetes; immune deficiency syndrome; HIV; AIDS; cerebral;
 KW spinal cord trauma injury; alopecia; ageing; Parkinson's disease;
 KW Alzheimer's disease; Down's syndrome; spinal muscular atrophy;
 KW multiple sclerosis; neurodegenerative disorders; caspase;
 KW gamma-ketoacid tetrapeptide; cysteine proteases.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "N-terminal acetyl"
 FT Modified-site 4
 FT /note= "D(CHO)"
 XX
 PN W0200032620-A1.
 XX
 PD 08-JUN-2000.
 XX
 PF 30-NOV-1999; 99WO-CA001145.
 XX
 PR 02-DEC-1998; 98US-0110567P.
 XX
 PA (MERI) MERCK FROSST CANADA & CO.
 XX
 PI Grimm EL, Renaud J, Aspiotis R, Bayly CI, Zamboni R, Black S;
 XX
 DR WPI; 2000-412282/35.
 XX
 PT New gamma-ketoacid tetrapeptide compounds having caspase-3 inhibiting
 PT activity, useful for treating e.g. Parkinson's disease, organ damage
 PT during transportation, alopecia and ageing.
 XX
 PS Disclosure; Page 4; 121pp; English.
 XX
 CC The present invention relates to gamma-ketoacid tetrapeptide compounds,
 CC which have been found to inhibit caspase-3. Inhibition of caspase
 CC activity is known to inhibit apoptosis. The present sequence is a
 CC tetrapeptide aldehyde which is a very potent inhibitor of caspase-3. This
 CC peptide was designed to mimic the caspase-3 recognition site (see
 CC AAY99957). Caspase-3 inhibitors may be used for treating cardiac and
 CC cerebral ischemia/reperfusion injury (e.g. stroke), type I diabetes,
 CC immune deficiency syndrome (e.g. HIV or AIDS), cerebral and spinal chord
 CC trauma injury, alopecia, ageing, Parkinson's disease, Alzheimer's
 CC disease, Down's syndrome, spinal muscular atrophy, multiple sclerosis and
 CC neurodegenerative disorders. They may also be used for treating other
 CC caspase-3 mediated diseases
 XX
 SQ Sequence 4 AA;
 Query Match 100.0%; Score 21; DB 3; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e-06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DEVD 4
 DB 1 DEVD 4
 ||||
 Search completed: May 24, 2004, 14:38:16
 Job time : 52 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 24, 2004, 14:36:17 ; Search time 16.5 Seconds
(without alignments)
12.515 Million cell updates/sec

Title: US-09-765-105A-2

Perfect score: 21

Sequence: 1 DEVD 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

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4: /cgn2_6/prodata/2/aa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	4	1	US-08-446-925-9
2	21	100.0	4	2	US-08-800-007A-10
3	21	100.0	4	2	US-09-146-331-9
4	21	100.0	4	2	US-08-915-414A-1
5	21	100.0	4	2	US-08-896-885-9
6	21	100.0	4	2	US-08-712-878-2
7	21	100.0	4	3	US-09-226-568-39
8	21	100.0	4	3	US-08-802-981-2
9	21	100.0	4	3	US-09-270-735-2
10	21	100.0	4	3	US-09-167-921-42
11	21	100.0	4	3	US-09-270-736-1
12	21	100.0	4	3	US-08-761-483-3
13	21	100.0	4	3	US-08-761-483-10
14	21	100.0	4	3	US-09-323-743-42
15	21	100.0	4	3	US-09-058-969-2
16	21	100.0	4	3	US-09-130-193-1
17	21	100.0	4	3	US-09-130-193-7
18	21	100.0	4	3	US-09-130-193-12
19	21	100.0	4	3	US-09-130-193-15
20	21	100.0	4	3	US-09-357-952-5
21	21	100.0	4	3	US-09-309-003-1
22	21	100.0	4	3	US/08/869
23	21	100.0	4	3	US-09-257-218-81
24	21	100.0	4	3	US-09-257-218-82
25	21	100.0	4	3	US-08-311-760-81
26	21	100.0	4	3	US-08-311-760-82
27	21	100.0	4	3	US-09-291-692-71

28 21 100.0 4 4 US-09-521-650-5 Sequence 5, Appl1
29 21 100.0 4 4 US-09-188-888-5 Sequence 5, Appl1
30 21 100.0 4 4 US-09-545-565-3 Sequence 3, Appl1
31 21 100.0 4 4 US-09-375-256-9 Sequence 9, Appl1
32 21 100.0 4 4 US-09-561-756-52 Sequence 52, Appl1
33 21 100.0 4 4 US-09-227-721-52 Sequence 52, Appl1
34 21 100.0 4 4 US-09-115-455-4 Sequence 4, Appl1
35 21 100.0 4 4 US-09-376-156-9 Sequence 9, Appl1
36 21 100.0 4 4 US-09-513-783A-60 Sequence 60, Appl1
37 21 100.0 4 4 US-08-865-579-81 Sequence 81, Appl1
38 21 100.0 4 4 US-08-865-579-82 Sequence 82, Appl1
39 21 100.0 4 4 US-09-495-120-1 Sequence 1, Appl1
40 21 100.0 4 4 US-09-353-215-4 Sequence 1, Appl1
41 21 100.0 4 4 US-09-649-810B-1 Sequence 4, Appl1
42 21 100.0 4 4 US-08-724-378D-17 Sequence 17, Appl1
43 21 100.0 4 4 US-08-842-760A-3 Sequence 3, Appl1
44 21 100.0 4 4 US-09-482-813-2 Sequence 2, Appl1
45 21 100.0 4 4 US-09-300-374-1 Sequence 1, Appl1

ALIGNMENTS

RESULT 1

US-08-446-925-9
; Sequence 9, Application US/08446925
; Patent No. 5672500
; GENERAL INFORMATION:
; APPLICANT: Litwack, Gerald
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: MCH2, AN APOPTOTIC CYSTEINE
; TITLE OF INVENTION: PROTEASE,
; TITLE OF INVENTION: AND COMPOSITIONS FOR MAKING AND
; TITLE OF INVENTION: METHODS
; TITLE OF INVENTION: OF USING THE SAME
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
; ADDRESSEE: No. 5672500ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,925
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJJ-1508
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-446-925-9

Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
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 Db 1 DEVD 4

RESULT 2
 US-08-800-007A-10
 ; Sequence 10, Application US/08800007A
 ; Patent No. 5834228
 ; GENERAL INFORMATION:
 ; APPLICANT: Becker, Joseph
 ; APPLICANT: Nicholson, Donald
 ; APPLICANT: Rotonda, Jennifer
 ; APPLICANT: Thornberry, Nancy
 ; APPLICANT: Fazil, Kimberly
 ; APPLICANT: Gallant, Michel
 ; APPLICANT: Gareau, Yves
 ; APPLICANT: Labelle, Marc
 ; APPLICANT: Peterson, Erin
 ; APPLICANT: Rasper, Dita
 ; TITLE OF INVENTION: CRYSTAL STRUCTURE OF APOPAIN
 ; TITLE OF INVENTION: AND USES THEREOF
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: JOSEPH A. COPPOLA - MERCK & CO., INC.
 ; STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
 ; CITY: RAHWAY
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 07065
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/800,007A
 ; FILING DATE: 13-FEB-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: COPPOLA, JOSEPH A
 ; REGISTRATION NUMBER: 38,413
 ; REFERENCE/DOCKET NUMBER: 19644
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 732-594-6734
 ; TELEFAX: 732-594-4720
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-800-007A-10

Query Match 100.0%; Score 21; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 1 DEVD 4
 ||||
 Db 1 DEVD 4

RESULT 3
 US-09-146-331-9
 ; Sequence 9, Application US/09146331
 ; Patent No. 5958720
 ; GENERAL INFORMATION:

; APPLICANT: Litwack, Gerald
 ; APPLICANT: Alnemri, Emad S.
 ; APPLICANT: Fernandez-Alnemri, Teresa
 ; TITLE OF INVENTION: Mch2, AN APOPTOTIC CYSTEINE
 ; TITLE OF INVENTION: PROTEASE AND COMPOSITIONS FOR MAKING AND
 ; TITLE OF INVENTION: METHODS OF USING THE SAME
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
 ; ADDRESSEE: No. 5958720ris
 ; STREET: One Liberty Place, 46th floor
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19103
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WordPerfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/146,331
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/896,885
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Deluca, Mark
 ; REGISTRATION NUMBER: 33,229
 ; REFERENCE/DOCKET NUMBER: TJU-1508
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (215) 568-3100
 ; TELEFAX: (215) 568-3439
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-146-331-9

Query Match 100.0%; Score 21; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
 ||||
 Db 1 DEVD 4

RESULT 4
 US-08-915-414A-1
 ; Sequence 1, Application US/08915414A
 ; Patent No. 5976822
 ; GENERAL INFORMATION:
 ; APPLICANT: LANDRUM, ET AL.
 ; TITLE OF INVENTION: METHOD AND REAGENT FOR MONITORING APOPTOSIS
 ; TITLE OF INVENTION: AND DISTINGUISHING APOPTOSIS FROM NECROSIS
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MITCHELL ALTER, COULTER INTERN. CORP.
 ; STREET: 11800 SW 147 AVE.
 ; CITY: MIAMI
 ; STATE: FLORIDA
 ; COUNTRY: USA
 ; ZIP: 33196
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
 ; COMPUTER: IBM PC
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: Microsoft Word 6.0/95
 ; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/915,414A
FILING DATE: 20-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/444,051
FILING DATE: 18-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: MITCHELL E. ALTER
REGISTRATION NUMBER: 28,684
TELECOMMUNICATION INFORMATION:
TELEPHONE: (305) 380-3636
TELEFAX: (305) 380-4566
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
US-08-915-414A-1

Query Match 100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
|||
Db 1 DEVD 4

RESULT 5
US-08-896-885-9
Sequence 9, Application US/08896885
Patent No. 5985640
GENERAL INFORMATION:
APPLICANT: Litwack, Gerald
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: Mch2, AN APOPTOTIC CYSTEINE
PROTEASE, AND COMPOSITIONS FOR MAKING AND
METHODS OF USING THE SAME
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
ADDRESSEE: No. 5985640ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,885
FILING DATE: 18-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/446,925
FILING DATE: 18-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1508
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-896-885-9
Query Match 100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DEVD 4
|||
Db 1 DEVD 4
RESULT 6
US-08-712-878-2
Sequence 2, Application US/08712878
Patent No. 5985863
GENERAL INFORMATION:
APPLICANT: Su, Michael
APPLICANT: Gu, Yong
APPLICANT: Livingston, David J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DECREASING
IGIF AND IFN-GAMMA PRODUCTION BY ADMINISTERING AN ICE
INHIBITOR
TITLE OF INVENTION: INHIBITOR
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr.
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10020

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,878
FILING DATE: 12-SEP-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: VFI/96-05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note="aspartic acid is
OTHER INFORMATION: acetylated"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /note="aspartic acid carboxy
OTHER INFORMATION: terminus is reduced to an aldehyde"
US-08-712-878-2

Query Match 100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
|
|
|
|
Db 1 DEVD 4

RESULT 7

US-09-226-568-39
; Sequence 39, Application US/09226568
; Patent No. 6001992
; GENERAL INFORMATION:
; APPLICANT: Ackermann, Elizabeth J.
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcuseon, Eric G.
; TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
; FILE REFERENCE: bcl-2-Related Proteins
; CURRENT FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-226-568-39

Query Match 100.0%; Score 21; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
|
|
|
|
Db 1 DEVD 4

RESULT 8

US-08-802-981-2
; Sequence 2, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,981
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-000300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-802-981-2

Query Match 100.0%; Score 21; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
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|
|
|
Db 1 DEVD 4

RESULT 9

US-09-270-735-2
; Sequence 2, Application US/09270735
; Patent No. 6135591
; GENERAL INFORMATION:
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Drewe, John
; APPLICANT: Wang, Yan
; APPLICANT: Weber, Eckard
; TITLE OF INVENTION: Dipeptide Caspase Inhibitors and the Use Thereof
; FILE REFERENCE: 1735.0010001
; CURRENT APPLICATION NUMBER: US/09/270,735
; CURRENT FILING DATE: 1999-03-16
; EARLIER APPLICATION NUMBER: 60/078,051
; EARLIER FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide
US-09-270-735-2

Query Match 100.0%; Score 21; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
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|
|
Db 1 DEVD 4

RESULT 10

US-09-167-921-42
; Sequence 42, Application US/09167921A
; Patent No. 6172216
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Nickoloff, Brian J.
; APPLICANT: Zhang, QingQing
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
; FILE REFERENCE: ISPH-0324
; CURRENT APPLICATION NUMBER: US/09/167,921A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: caspase assay substrate

US-09-167-921-42

Query Match 100.0%; Score 21; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
 ||||
DB 1 DEVD 4

RESULT 11

US-09-270-736-1
; Sequence 1, Application US/09270736
; Patent No. 6184210
; GENERAL INFORMATION:
; APPLICANT: Keana, John F.W.
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Guastella, John
; APPLICANT: Yang, Wu
; APPLICANT: Drewe, John A.
; APPLICANT: Weber, Eckard
; TITLE OF INVENTION: Dipeptide Apoptosis Inhibitors and the Use Thereof
; FILE REFERENCE: 1735.0280002
; CURRENT APPLICATION NUMBER: US/09/270,736
; CURRENT FILING DATE: 1999-03-16
; EARLIER APPLICATION NUMBER: US 09/168,945
; EARLIER FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,676
; EARLIER FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide

US-09-270-736-1

Query Match 100.0%; Score 21; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
 ||||
DB 1 DEVD 4

RESULT 12

US-08-761-483-3
; Sequence 3, Application US/08761483
; Patent No. 6204261
; GENERAL INFORMATION:
; APPLICANT: Batchelor, Mark J
; APPLICANT: Bebbington, David
; APPLICANT: Bemis, Guy W
; APPLICANT: Fridman, Wolf H
; APPLICANT: Gillespie, Roger J
; APPLICANT: Golec, Julian MC
; APPLICANT: Gu, Yong
; APPLICANT: Lauffer, David J
; APPLICANT: Livingston, David J
; APPLICANT: Matharu, Saroop S
; TITLE OF INVENTION: INHIBITORS OF INTERLEUKIN-1 BETA
; TITLE OF INVENTION: CONVERTING ENZYME
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York

COUNTRY: USA

ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/761.483

FILING DATE: 06-DEC-1996

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Haley Jr, James F

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: VPI/36-01CIP2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-596-9000

TELEFAX: 212-596-9090

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1

OTHER INFORMATION: /note= "Aspartic acid is

OTHER INFORMATION: acetylated"

FEATURE:

NAME/KEY: Modified-site

LOCATION: 4

OTHER INFORMATION: /note= "aspartic acid terminal acid

OTHER INFORMATION: is reduced to an aldehyde"

US-08-761-483-3

Query Match

100.0%; Score 21; DB 3; Length 4;

Best Local Similarity

100.0%; Pred. No. 3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4

DB 1 DEVD 4

RESULT 13

US-08-761-483-10

; Sequence 10, Application US/08761483

; Patent No. 6204261

; GENERAL INFORMATION:

; APPLICANT: Batchelor, Mark J

; APPLICANT: Bebbington, David

; APPLICANT: Bemis, Guy W

; APPLICANT: Fridman, Wolf H

; APPLICANT: Gillespie, Roger J

; APPLICANT: Golec, Julian MC

; APPLICANT: Gu, Yong

; APPLICANT: Lauffer, David J

; APPLICANT: Livingston, David J

; APPLICANT: Matharu, Saroop S

; TITLE OF INVENTION: INHIBITORS OF INTERLEUKIN-1 BETA

; TITLE OF INVENTION: CONVERTING ENZYME

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Neave

; STREET: 1251 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10020

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/761,493
FILING DATE: 06-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: VPI/96-01CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /note="aspartic acid is
OTHER INFORMATION: derivatized with amino-4-methylcoumarin"
US-08-761-483-10

Query Match 100.0%; Score 21; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
Db 1 DEVD 4

RESULT 14
US-09-323-743-42
Sequence 42, Application US/09323743
Patent No. 6214386
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett P.
APPLICANT: Nickoloff, Brian J.
APPLICANT: Zhang, QingQing
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
FILE REFERENCE: ISPH-0368
CURRENT APPLICATION NUMBER: US/09/323,743
CURRENT FILING DATE: 1999-06-01
EARLIER APPLICATION NUMBER: 09/277,020
EARLIER FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 09/167,921
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 42
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-323-743-42

Query Match 100.0%; Score 21; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
Db 1 DEVD 4
RESULT 15
US-09-058-969-2
Sequence 2, Application US/09058969A
Patent No. 6228603
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Deveraux, Quinn
APPLICANT: Salvesen, Guy S.
APPLICANT: Takahashi, Ryosuke
APPLICANT: Roy, Natalie
TITLE OF INVENTION: Screening Assays For Agents That Alter Inhibitor of
Apoptosis (IAP) Protein Regulation of Caspase Activity
FILE REFERENCE: LJ 3080
CURRENT APPLICATION NUMBER: US/09/058,969A
CURRENT FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 08/862,087
EARLIER FILING DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 4
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Consensus Sequence
US-09-058-969-2

Query Match 100.0%; Score 21; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
Db 1 DEVD 4

Search completed: May 24, 2004, 14:39:00
Job time : 17.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 24, 2004, 14:39:37 ; Search time 38 Seconds
(without alignments)
29,360 Million cell updates/sec

Title: US-09-765-105A-2

Perfect score: 21
Sequence: 1 DEVD 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1149313 seqs, 278921704 residues

Total number of hits satisfying chosen parameters: 1149313

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA:*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCF_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/PCFUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
 - 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	4	9	US-09-045-620-4
2	21	100.0	4	9	US-09-734-846-42
3	21	100.0	4	9	US-09-799-463-2
4	21	100.0	4	9	US-09-735-363A-85
5	21	100.0	4	9	US-09-799-994-2
6	21	100.0	4	9	US-09-352-768-71
7	21	100.0	4	9	US-09-858-754-11
8	21	100.0	4	9	US-09-387-417-3
9	21	100.0	4	9	US-09-737-255-1
10	21	100.0	4	9	US-09-920-332-1
11	21	100.0	4	9	US-09-845-028-8
12	21	100.0	4	9	US-09-954-697-52
13	21	100.0	4	9	US-09-347-387-5
14	21	100.0	4	10	US-09-161-172-2
15	21	100.0	4	10	US-09-866-512A-7

16	21	100.0	4	10	US-09-862-224-1	Sequence 1, Appli
17	21	100.0	4	12	US-10-227-012-8	Sequence 8, Appli
18	21	100.0	4	12	US-10-182-975-3	Sequence 3, Appli
19	21	100.0	4	12	US-10-452-184-1	Sequence 1, Appli
20	21	100.0	4	12	US-10-668-955-71	Sequence 71, Appl
21	21	100.0	4	12	US-09-746-731-81	Sequence 81, Appl
22	21	100.0	4	12	US-09-746-731-82	Sequence 82, Appl
23	21	100.0	4	12	US-09-765-105-2	Sequence 2, Appli
24	21	100.0	4	12	US-09-780-142-3	Sequence 3, Appli
25	21	100.0	4	12	US-09-863-649-2	Sequence 2, Appli
26	21	100.0	4	12	US-09-270-983-9	Sequence 9, Appli
27	21	100.0	4	12	US-09-819-266-1	Sequence 1, Appli
28	21	100.0	4	12	US-10-099-408A-3	Sequence 3, Appli
29	21	100.0	4	12	US-10-146-138A-1	Sequence 1, Appli
30	21	100.0	4	12	US-10-151-119B-1	Sequence 1, Appli
31	21	100.0	4	12	US-10-168-447-5	Sequence 5, Appli
32	21	100.0	4	12	US-10-356-665-1	Sequence 1, Appli
33	21	100.0	4	13	US-10-103-448-6	Sequence 6, Appli
34	21	100.0	4	13	US-10-059-749-81	Sequence 81, Appl
35	21	100.0	4	13	US-10-059-749-82	Sequence 82, Appl
36	21	100.0	4	13	US-10-108-929-6	Sequence 6, Appli
37	21	100.0	4	14	US-10-141-769-1	Sequence 1, Appli
38	21	100.0	4	14	US-10-171-077-9	Sequence 9, Appli
39	21	100.0	4	14	US-10-171-417-7	Sequence 7, Appli
40	21	100.0	4	14	US-10-164-705-1	Sequence 1, Appli
41	21	100.0	4	14	US-10-158-827-1	Sequence 1, Appli
42	21	100.0	4	14	US-10-105-779-1	Sequence 1, Appli
43	21	100.0	4	14	US-10-066-805A-1	Sequence 1, Appli
44	21	100.0	4	14	US-10-244-586-12	Sequence 12, Appl
45	21	100.0	4	14	US-10-100-957A-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1
US-09-045-620-4
; Sequence 4, Application US/09045620
; Patent No. US20010006793A1
; GENERAL INFORMATION:
; APPLICANT: BJORNSTI, Mary-Ann
; APPLICANT: KANG, David
; APPLICANT: KANG, Jason
; TITLE OF INVENTION: MODULATORS OF EUKARYOTIC CASPASES
; FILE REFERENCE: 209855.0037/27US
; CURRENT APPLICATION NUMBER: US/09/045.620
; CURRENT FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fluorometric
; OTHER INFORMATION: caspase-specific peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)
; OTHER INFORMATION: aminomethyl coumarin linked with residue 4
US-09-045-620-4

Query Match 100.0%; Score 21; DB 9; Length 4;
Best Local Similarity 100.0%; Pred.No.1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
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Db 1 DEVD 4

RESULT 2
US-09-734-846-42


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; Sequence 42, Application US/09734846
; Patent No. US20010007025A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Nickoloff, Brian J.
; APPLICANT: Zhang, QingGong
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
; FILE REFERENCE: ISPH-0528
; CURRENT APPLICATION NUMBER: US/09/734,846
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 09/277,020
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 09/167,921
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 09/323,743
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-734-846-42

Query Match 100.0%; Score 21; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
Db 1 DEVD 4

RESULT 3
US-09-799-463-2
; Sequence 2, Application US/09799463
; Patent No. US20010018195A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Devereaux, Quinn
; APPLICANT: Salvesen, Guy S.
; APPLICANT: Takahashi, Ryosuke
; APPLICANT: Roy, Natalie
; TITLE OF INVENTION: Screening Assays For Agents That Alter Inhibitor of
; FILE REFERENCE: LJ 3080
; CURRENT APPLICATION NUMBER: US/09/799,463
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 09/058,969
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 08/862,087
; PRIOR FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:Consensus Sequence
US-09-799-463-2

Query Match 100.0%; Score 21; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
Db 1 DEVD 4

RESULT 4
US-09-735-363A-85
; Sequence 85, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Filion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 85
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; US-09-735-363A-85

Query Match 100.0%; Score 21; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
Db 1 DEVD 4

RESULT 5
US-09-799-994-2
; Sequence 2, Application US/09799994
; Patent No. US20020009757A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Devereaux, Quinn
; APPLICANT: Salvesen, Guy S.
; APPLICANT: Takahashi, Ryosuke
; APPLICANT: Roy, Natalie
; TITLE OF INVENTION: Screening Assays For Agents That Alter Inhibitor of
; FILE REFERENCE: LJ 3080
; CURRENT APPLICATION NUMBER: US/09/799,994
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 09/058,969
; PRIOR FILING DATE: 1998-04-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:Consensus Sequence
US-09-799-994-2

Query Match 100.0%; Score 21; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
Db 1 DEVD 4

RESULT 6
US-09-799-994-2
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US-09-952-768-71
; Sequence 71, Application US/09952768
; Patent No. US20020035242A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
;               Fernandes-Alnemri, Teresa
;               Litwack, Gerald
;               Armstrong, Robert
;               Tomaselli, Kevin
; TITLE OF INVENTION: MCH4 AND MCH5. APOPTOTIC PROTEASE.
;               NUCLEIC ACIDS ENCODING AND METHODS OF USE
;
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: Suite 6300, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent'n Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/952,768
; FILING DATE: 10-Sep-2001
; CLASSIFICATION: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Christiansen, William T.
; REGISTRATION NUMBER: 44,614
; REFERENCE/DOCKET NUMBER: 480140.424C4
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
;
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 71:
US-09-952-768-71

Query Match          100.0%; Score 21; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. NO. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1      DEVD 4
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DB      1      DEVD 4

RESULT 7
US-09-858-754-11
; Sequence 11, Application US/09858754
; Patent No. US2002005130A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Gary L.
; TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING APOPTOSIS
; FILE REFERENCE: CPI-042
; CURRENT APPLICATION NUMBER: US/09/858,754
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/023,130
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/039,740
; PRIOR FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 4
; TYPE: PRT
; ORGANISM: synthetic construct

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Qy      1 DEVD 4
Db      1 DEVD 4

RESULT 10
US-09-920-332-1
; Sequence 1, Application US/09920332
; Patent No. US2002007673A1
; GENERAL INFORMATION:
; APPLICANT: Kasibhatla, Shailaja
; APPLICANT: Green, Douglas R.
; APPLICANT: Tseng, Ben
; TITLE OF INVENTION: Method of Identifying Immunosuppressive Agents
; FILE REFERENCE: 1735.0470001/RWE/ALS
; CURRENT APPLICATION NUMBER: US/09/920,332
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/422,897
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Fluorogenic substrate
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
US-09-920-332-1
Query Match      100.0%; Score 21; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DEVD 4
Db      1 DEVD 4

RESULT 11
US-09-845-028-8
; Sequence 8, Application US/09845028
; Patent No. US20020081705A1
; GENERAL INFORMATION:
; APPLICANT: Mankovich, John
; TITLE OF INVENTION: HUMAN CASPASE-14 COMPOSITIONS
; FILE REFERENCE: BSI-111
; CURRENT APPLICATION NUMBER: US/09/845,028
; CURRENT FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/199,962
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-028-8
Query Match      100.0%; Score 21; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DEVD 4
Db      1 DEVD 4

RESULT 12
US-09-954-697-52
; Sequence 52, Application US/09954697
; Patent No. US20020106631A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
; FILE REFERENCE: 480140.431D2
; CURRENT APPLICATION NUMBER: US/09/954,697
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 52
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-954-697-52
Query Match      100.0%; Score 21; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DEVD 4
Db      1 DEVD 4

RESULT 13
US-09-947-387-5
; Sequence 5, Application US/09947387
; Patent No. US20020150895A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. US20020150895A1el Fluorogenic or Fluorescent Reporter Molecu
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; FILE REFERENCE: 1735.0290005
; CURRENT APPLICATION NUMBER: US/09/947,387
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/061,582
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: US 60/145,746
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: US 09/168,888
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-947-387-5
Query Match      100.0%; Score 21; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DEVD 4
Db      1 DEVD 4

RESULT 14
US-09-161-172-2
; Sequence 2, Application US/09161172
; Publication No. US20030044776A1
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Db 1 DEVD 4
Search completed: May 24, 2004, 14:49:5
Job time : 38 secs

GENERAL INFORMATION:
; APPLICANT: Dykens, James A.
; APPLICANT: Miller, Scott W.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
; TITLE OF INVENTION: AGENTS THAT ALTER MITOCHONDRIAL PERMEABILITY
; TITLE OF INVENTION: TRANSITION PORES
; FILE REFERENCE: 660088.418
; CURRENT APPLICATION NUMBER: US/09/161,172
; CURRENT FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: caspase-3 specific fluorogenic peptide substrate
US-09-161-172-2

Query Match 100.0%; Score 21; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DEVD 4
Db 1 DEVD 4

RESULT 15
US-09-866-512A-7
; Sequence 7, Application US/09866512A
; Publication No. US2003053954A1
; GENERAL INFORMATION:
; APPLICANT: Meade, Thomas J
; TITLE OF INVENTION: Magnetic Resonance Imaging Agents for the Detection of Physiological
; TITLE OF INVENTION: Agents
; FILE REFERENCE: A-58634-7
; CURRENT APPLICATION NUMBER: US/09/866,512A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/287,619
; PRIOR FILING DATE: 2001-05-26
; PRIOR APPLICATION NUMBER: US 08/460,511
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: US 08/486,968
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/971,855
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 09/134,072
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 09/866,512
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 09/405,046
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/063,328
; PRIOR FILING DATE: 1997-10-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: could be from any mammal.
US-09-866-512A-7

Query Match 100.0%; Score 21; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DEVD 4
Db 1 DEVD 4

Agg
Res

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 24, 2004, 14:38:22 ; Search time 175 Seconds
(without alignments)
22.310 Million cell updates/sec

Title: US-09-765-105A-2

Perfect score: 21

Sequence: 1 DEVD 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6019581 seqs, 976053577 residues

Total number of hits satisfying chosen parameters: 6019581

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
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- 27: /cgn2_6/ptodata/2/paa/US101_COMB.pep.*
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- 31: /cgn2_6/ptodata/2/paa/US106_COMB.pep.*
- 32: /cgn2_6/ptodata/2/paa/US107_COMB.pep.*
- 33: /cgn2_6/ptodata/2/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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RESULT 1
PCT-US00-02329-1
; Sequence 1, Application PC/TUS0002329
; GENERAL INFORMATION:
; APPLICANT: Cytovia, Inc.
; TITLE OF INVENTION: Methods of Identifying Potentially Therapeutically Effective Antineoplastic Agents with Viable Cultured Cells Having an Intact Cell Membrane and Product by
; TITLE OF INVENTION: Cells Having an Intact Cell Membrane and Product by
; TITLE OF INVENTION: Same
; FILE REFERENCE: 1735.032PC02
; CURRENT APPLICATION NUMBER: PCT/US00/02329
; CURRENT FILING DATE: 2000-02-01
; EARLIER APPLICATION NUMBER: 60/118,102
; EARLIER FILING DATE: 1999-02-01
; EARLIER APPLICATION NUMBER: 09/454,595
; EARLIER FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

ALIGNMENTS

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2	21	100.0	4	1	PCT-US00-02329-1	Sequence 1, Appli
3	21	100.0	4	1	PCT-US00-09319-3	Sequence 3, Appli
4	21	100.0	4	1	PCT-US00-14451-42	Sequence 42, Appli
5	21	100.0	4	1	PCT-US01-04137-1	Sequence 1, Appli
6	21	100.0	4	1	PCT-US01-48256-1	Sequence 1, Appli
7	21	100.0	4	1	PCT-US02-04060-52	Sequence 52, Appli
8	21	100.0	4	1	PCT-US02-07569-1	Sequence 1, Appli
9	21	100.0	4	1	PCT-US02-14722-1	Sequence 1, Appli
10	21	100.0	4	1	PCT-US02-15386-1	Sequence 1, Appli
11	21	100.0	4	1	PCT-US02-15401-1	Sequence 1, Appli
12	21	100.0	4	1	PCT-US02-15713-1	Sequence 1, Appli
13	21	100.0	4	1	PCT-US02-17108-1	Sequence 1, Appli
14	21	100.0	4	1	PCT-US02-17486-1	Sequence 1, Appli
15	21	100.0	4	1	PCT-US02-17892-1	Sequence 1, Appli
16	21	100.0	4	1	PCT-US02-18014-8	Sequence 8, Appli
17	21	100.0	4	1	PCT-US02-24119-22	Sequence 22, Appli
18	21	100.0	4	1	PCT-US02-37577-2	Sequence 2, Appli
19	21	100.0	4	1	PCT-US03-02520-7	Sequence 7, Appli
20	21	100.0	4	1	PCT-US03-05221-1	Sequence 1, Appli
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22	21	100.0	4	1	PCT-US03-15432-1	Sequence 1, Appli
23	21	100.0	4	1	PCT-US03-20668-1	Sequence 1, Appli
24	21	100.0	4	1	PCT-US03-20997-1	Sequence 1, Appli
25	21	100.0	4	1	PCT-US96-07010-9	Sequence 9, Appli
26	21	100.0	4	1	PCT-US98-12716-27	Sequence 27, Appli
27	21	100.0	4	1	PCT-US98-21231-5	Sequence 5, Appli
28	21	100.0	4	1	PCT-US99-08064-37	Sequence 37, Appli
29	21	100.0	4	1	PCT-US99-16423-5	Sequence 5, Appli
30	21	100.0	4	1	PCT-US99-22448-42	Sequence 42, Appli
31	21	100.0	4	1	PCT-US99-29593-39	Sequence 39, Appli
32	21	100.0	4	10	US-08-689-583-2	Sequence 2, Appli
33	21	100.0	4	11	US-08-715-031-56	Sequence 56, Appli
34	21	100.0	4	13	US-08-902-766-13	Sequence 13, Appli
35	21	100.0	4	13	US-08-918-674-1	Sequence 1, Appli
36	21	100.0	4	13	US-08-948-124-3	Sequence 3, Appli
37	21	100.0	4	14	US-09-021-130-11	Sequence 11, Appli
38	21	100.0	4	14	US-09-026-716-15	Sequence 15, Appli
39	21	100.0	4	14	US-09-045-620-4	Sequence 4, Appli
40	21	100.0	4	14	US-09-099-463-27	Sequence 27, Appli
41	21	100.0	4	14	US-09-099-463A-27	Sequence 27, Appli
42	21	100.0	4	15	US-09-161-172-2	Sequence 2, Appli
43	21	100.0	4	16	US-09-243-286A-1	Sequence 1, Appli
44	21	100.0	4	16	US-09-270-983-9	Sequence 9, Appli
45	21	100.0	4	16	US-09-296-682-1	Sequence 1, Appli

; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
PCT-US00-02329-1

Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 DEVD 4

RESULT 2

PCT-US00-02332-1
; Sequence 1, Application PC/TUS0002332
; GENERAL INFORMATION:
; APPLICANT: CYTOVIA, INC.
; APPLICANT: CAI, SUI XIONG
; APPLICANT: ZHANG, HAN-ZHONG
; APPLICANT: WANG, YAN
; APPLICANT: TSENG, BEN
; APPLICANT: KASIBHATLA, SHAILAJA
; APPLICANT: DREWE, JOHN A.
; TITLE OF INVENTION: GAMBOGIC ACID, ANALOGS AND DERIVATIVES AS ACTIVATORS OF
; FILE REFERENCE: 1735.032PC03
; CURRENT APPLICATION NUMBER: PCT/US00/02332
; CURRENT FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
PCT-US00-02332-1

Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
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Db 1 DEVD 4

RESULT 3

PCT-US00-09319-3
; Sequence 3, Application PC/TUS0009319
; GENERAL INFORMATION:
; APPLICANT: Cytovia, Inc.
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Weber, Eckard
; APPLICANT: Wang, Yan
; APPLICANT: Mills, Gordon B.
; APPLICANT: Green, Douglas R.
; TITLE OF INVENTION: Caspase Inhibitors and the Use Thereof
; FILE REFERENCE: 1735.035PC02
; CURRENT APPLICATION NUMBER: PCT/US00/09319
; CURRENT FILING DATE: 2000-04-07
; EARLIER APPLICATION NUMBER: US 60/128,545
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: US 60/158,370
; EARLIER FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Caspase
; OTHER INFORMATION: inhibitor

; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: caspase 3
; OTHER INFORMATION: substrate
PCT-US00-09319-3

Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
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Db 1 DEVD 4

RESULT 4

PCT-US00-14451-42
; Sequence 42, Application PC/TUS0014451
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Nickoloff, Brian J.
; APPLICANT: Zhang, QingQing
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
; FILE REFERENCE: ISPH-0460
; CURRENT APPLICATION NUMBER: PCT/US00/14451
; CURRENT FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/323,743
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: 09/167,921
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 09/277,020
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 42
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
PCT-US00-14451-42

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Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
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Db 1 DEVD 4

RESULT 5

PCT-US01-04137-1
; Sequence 1, Application PC/TUS0104137
; GENERAL INFORMATION:
; APPLICANT: Alexion Pharmaceuticals, Inc.
; APPLICANT: Fodor, William L.
; TITLE OF INVENTION: MIXTURES OF CASPASE INHIBITORS AND COMPLEMENT
; FILE REFERENCE: 1087-15PCT
; CURRENT APPLICATION NUMBER: PCT/US01/04137
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Caspase
; OTHER INFORMATION: inhibitor

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PCT-US01-04137-1
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Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DEVD 4
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Db      1 DEVD 4

RESULT 6
PCT-US01-48256-1
; Sequence 1, Application PC/TUS0148256
; GENERAL INFORMATION:
; APPLICANT: Regents of the University of Michigan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
; TITLE OF INVENTION: PROTEOLYTIC ACTIVITY
; FILE REFERENCE: 11203-003W01
; CURRENT APPLICATION NUMBER: PCT/US01/48256
; PRIOR FILING DATE: 2001-12-13
; PRIOR APPLICATION NUMBER: 09/737,255
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-48256-1

Query Match      100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DEVD 4
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Db      1 DEVD 4

RESULT 7
PCT-US02-04060-52
; Sequence 52, Application PC/TUS0204060
; GENERAL INFORMATION:
; APPLICANT: Massachusetts Institute of Technology, et al.
; TITLE OF INVENTION: Peptides that Inhibit Poly-Glutamine Aggregation
; FILE REFERENCE: M0656/7062W0 (GRV)
; CURRENT APPLICATION NUMBER: PCT/US02/04060
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,898
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/334,891
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Caspase Inhibitor
PCT-US02-04060-52

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Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 DEVD 4

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PCT-US01-48256-1
; Sequence 1, Application PC/TUS0148256
; GENERAL INFORMATION:
; APPLICANT: Regents of the University of Michigan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
; TITLE OF INVENTION: PROTEOLYTIC ACTIVITY
; FILE REFERENCE: 11203-003W01
; CURRENT APPLICATION NUMBER: PCT/US01/48256
; PRIOR FILING DATE: 2001-12-13
; PRIOR APPLICATION NUMBER: 09/737,255
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-48256-1

Query Match      100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DEVD 4
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Db      1 DEVD 4

RESULT 9
PCT-US02-14722-1
; Sequence 1, Application PC/TUS0214722
; GENERAL INFORMATION:
; APPLICANT: Cytovia, Inc.
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Kasibhatla, Shailaja
; APPLICANT: Drewe, John
; APPLICANT: Reddy, P. Sanjeeva
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: Substituted N'-(Arylcabonyl)-Benzhydrazides,
; TITLE OF INVENTION: N'-(Arylcabonyl)-Benzylidene-hydrazides And Analogs as Activators of
; TITLE OF INVENTION: Caspases and Inducers of Apoptosis And The Use Thereof
; FILE REFERENCE: 1735.056PC01
; CURRENT APPLICATION NUMBER: PCT/US02/14722
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/289,803
; PRIOR FILING DATE: 2001-05-10
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fluorogenic substrate
PCT-US02-14722-1

Query Match      100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DEVD 4
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Db      1 DEVD 4

RESULT 10
PCT-US02-15398-1
; Sequence 1, Application PC/TUS0215398
; GENERAL INFORMATION:
; APPLICANT: CYTOVIA, INC.
; APPLICANT: CAI, SUI XIONG
PCT-US02-07569-1
; Sequence 1, Application PC/TUS0207569
; GENERAL INFORMATION:
; APPLICANT: Cytovia, Inc.
; TITLE OF INVENTION: Multifluoro-substituted Chalcones and Analogs as Activators of
; TITLE OF INVENTION: and Inducers of Apoptosis and the Use Thereof
; FILE REFERENCE: 1735.054PC01
; CURRENT APPLICATION NUMBER: PCT/US02/07569
; CURRENT FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/275,473
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fluorogenic Substrate
PCT-US02-07569-1

Query Match      100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DEVD 4
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Db      1 DEVD 4
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; APPLICANT: XU, LIPEN
; APPLICANT: STORER, RICHARD
; APPLICANT: ATTARDO, GIORGIO
; TITLE OF INVENTION: 7-8-FUSED 4H-CHROMENE AND ANALOGS AS ACTIVATORS OF CASPASES AND I
; TITLE OF INVENTION: OF APOPTOSIS AND THE USE THEREOF
; FILE REFERENCE: 1735.065PC01
; CURRENT APPLICATION NUMBER: PCT/US02/15398
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/290,976
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fluorogenic substrate
PCT-US02-15398-1

Query Match          100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
DB 1 DEVD 4

RESULT 11
PCT-US02-15401-1
; Sequence 1, Application PC/TUS0215401
; GENERAL INFORMATION:
; APPLICANT: Cytovia, Inc.
; APPLICANT: Shire BioChem, Inc.
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Zhang, Hong
; APPLICANT: Kemnitz, William E.
; APPLICANT: Jiang, Songchun
; APPLICANT: Drewe, John A.
; APPLICANT: Storer, Richard
; TITLE OF INVENTION: Substituted Coumarins and Quinolines and Analogs as Activators of
; TITLE OF INVENTION: Caspases and the Use Thereof
; FILE REFERENCE: 1735.066PC01
; CURRENT APPLICATION NUMBER: PCT/US02/15401
; CURRENT FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fluorogenic substrate
PCT-US02-15401-1

Query Match          100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
DB 1 DEVD 4

RESULT 12
PCT-US02-15713-1
; Sequence 1, Application PC/TUS0215713
; GENERAL INFORMATION:
; APPLICANT: PE CORPORATION (NY)
; APPLICANT: YAN, Xiongwei
; APPLICANT: MIRAGLIA, Sheri
; APPLICANT: YUAN, Pau M
; APPLICANT: XU, LIPEN
; APPLICANT: STORER, RICHARD
; APPLICANT: ATTARDO, GIORGIO
; TITLE OF INVENTION: 7-8-FUSED 4H-CHROMENE AND ANALOGS AS ACTIVATORS OF CASPASES AND I
; TITLE OF INVENTION: OF APOPTOSIS AND THE USE THEREOF
; FILE REFERENCE: 1735.065PC01
; CURRENT APPLICATION NUMBER: PCT/US02/15398
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/290,976
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fluorogenic substrate
PCT-US02-15398-1

Query Match          100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
DB 1 DEVD 4

RESULT 13
PCT-US02-17108-1
; Sequence 1, Application PC/TUS0217108
; GENERAL INFORMATION:
; APPLICANT: Cytovia, Inc.
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Nguyen, Bao Ngoc
; APPLICANT: Drewe, John
; APPLICANT: Reddy, P. Sanjeeva
; APPLICANT: Kasibhatla, Shailaja
; APPLICANT: Pervin, Azra
; TITLE OF INVENTION: 4-Substituted-1-(arylmethylidene)thiosemicarbazide,
; TITLE OF INVENTION: 4-Substituted-1-(arylcarbonyl)thiosemicarbazide and
; TITLE OF INVENTION: Analogs as Activators of Caspases and Inducers of
; TITLE OF INVENTION: Apoptosis and the Use Thereof
; FILE REFERENCE: 1735.060PC01
; CURRENT APPLICATION NUMBER: PCT/US02/17108
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/294,641
; PRIOR FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fluorogenic substrate
PCT-US02-17108-1

Query Match          100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
DB 1 DEVD 4

RESULT 14
PCT-US02-17486-1
; Sequence 1, Application PC/TUS0217486
; GENERAL INFORMATION:
; APPLICANT: Cytovia, Inc.
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Drewe, John
; APPLICANT: Kasibhatla, Shailaja
; TITLE OF INVENTION: Substituted 4-Aryl-3-(3-Aryl-1-Oxo-2-Propenyl)-2(1H)-Quinolone
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Job time : 176 secs

; TITLE OF INVENTION: Analogs as Activators of Caspases and Inducers of Apoptosis and
; FILE REFERENCE: 1735.057PC01
; CURRENT APPLICATION NUMBER: PCT/US02/17486
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/295,007
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fluorogenic substrate
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (4)..(4)
; OTHER INFORMATION:
; PCT-US02-17486-1

Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
Db 1 DEVD 4

RESULT 15
PCT-US02-17892-1
; Sequence 1, Application PC/TUS0217892
; GENERAL INFORMATION:
; APPLICANT: Cytovia, Inc.
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Drewe, John A.
; APPLICANT: Reddy, P. Sanjeeva
; APPLICANT: Kasibhatla, Shailaja
; APPLICANT: Roemerle, Jared Daniel
; APPLICANT: Ollis, Kristin P.
; TITLE OF INVENTION: Substituted 3-Aryl-5-aryl-[1,2,4]-oxadiazoles and
; TITLE OF INVENTION: Analogs as Activators of Caspases and Inducers of
; TITLE OF INVENTION: Apoptosis and the Use Thereof
; FILE REFERENCE: 1735.064PC01
; CURRENT APPLICATION NUMBER: PCT/US02/17892
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 60/296,479
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fluorogenic substrate
; PCT-US02-17892-1

Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
Db 1 DEVD 4

Search completed: May 24, 2004, 14:47:42

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 24, 2004, 14:39:07 ; Search time 13.5 seconds
(without alignments)
10.992 Million cell updates/sec

Title: US-09-765-105A-2
Perfect score: 21
Sequence: 1 DEVD 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 251736 seqs, 37097828 residues

Total number of hits satisfying chosen parameters: 251736

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA New.*

- 1: /cgn2_6/prodata/1/paa/PCT_NEW_COMB.pep.*
- 2: /cgn2_6/prodata/1/paa/US06_NEW_COMB.pep.*
- 3: /cgn2_6/prodata/1/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/prodata/1/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/prodata/1/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/prodata/1/paa/US10_NEW_COMB.pep.*
- 7: /cgn2_6/prodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	4	1	PCT-US03-20668A-1
2	21	100.0	4	1	PCT-US04-11915-41
3	21	100.0	4	1	PCT-US04-11916-23
4	21	100.0	4	6	US-10-768-976-64
5	21	100.0	4	6	US-10-530-926-14
6	21	100.0	4	6	US-10-826-905-43
7	21	100.0	4	6	US-10-626-258-22
8	21	100.0	4	6	US-10-471-720-1
9	21	100.0	4	6	US-10-030-378-1
10	21	100.0	4	6	US-10-263-330A-43
11	21	100.0	4	6	US-10-146-136-1
12	21	100.0	4	6	US-10-826-905A-43
13	21	100.0	4	6	US-10-826-893-1
14	21	100.0	4	6	US-10-826-909-41
15	21	100.0	4	6	US-10-826-923-23
16	21	100.0	4	6	US-10-829-381-5
17	21	100.0	4	6	US-10-844-470-39
18	21	100.0	4	7	US-60-549-602-4
19	21	100.0	5	1	PCT-US04-04752-15
20	21	100.0	5	1	PCT-US04-04752-19
21	21	100.0	5	6	US-10-884-346-41
22	21	100.0	5	6	US-10-884-346-42
23	21	100.0	5	6	US-10-829-381-76
24	21	100.0	7	1	PCT-US04-11915-42
25	21	100.0	7	1	PCT-US04-11915-44
26	21	100.0	7	1	PCT-US04-11916-24

27	21	100.0	7	1	PCT-US04-11916-26
28	21	100.0	7	5	US-09-394-019B-196
29	21	100.0	7	5	US-09-394-019B-198
30	21	100.0	7	5	US-09-394-019B-208
31	21	100.0	7	5	US-09-394-019B-193
32	21	100.0	7	5	US-09-394-019B-195
33	21	100.0	7	5	US-09-394-019B-205
34	21	100.0	7	5	US-09-394-019C-196
35	21	100.0	7	5	US-09-394-019C-198
36	21	100.0	7	5	US-09-394-019C-208
37	21	100.0	7	6	US-10-826-909-42
38	21	100.0	7	6	US-10-826-909-44
39	21	100.0	7	6	US-10-826-923-24
40	21	100.0	7	6	US-10-826-923-26
41	21	100.0	7	6	US-10-466-552A-1
42	21	100.0	8	5	US-09-394-019B-189
43	21	100.0	8	5	US-09-394-019B-197
44	21	100.0	8	5	US-09-394-019B-186
45	21	100.0	8	5	US-09-394-019B-194

ALIGNMENTS

RESULT 1
PCT-US03-20668A-1
; Sequence 1, Application PC/TUS0320668A
; GENERAL INFORMATION:
; APPLICANT: CVTOVIA, INC.
; APPLICANT: CAI, SUI XIONG
; APPLICANT: TSENG, BEN
; APPLICANT: ZHANG, HAN-ZHONG
; APPLICANT: KASIBHATLA, SHAILAJA
; APPLICANT: OLLIS, KRISTIN P.
; APPLICANT: SIRISOVA, NILANTHA SUDATH
; APPLICANT: DREWE, JOHN A.
; TITLE OF INVENTION: Derivatives of Gambogic Acid And Analogs As Activators of
; TITLE OF INVENTION: Caspases and Inducers of Apoptosis
; FILE REFERENCE: 1735.078PC02
; CURRENT APPLICATION NUMBER: PCT/US03/20668A
; CURRENT FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: 60/392,358
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/413,649
; PRIOR FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal acetyl
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: C-terminal N'-ethoxycarbonyl-Rhodamine 110
PCT-US03-20668A-1

Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
Db 1 DEVD 4

RESULT 2
PCT-US04-11915-41
; Sequence 41, Application PC/TUS0411915

```

; GENERAL INFORMATION:
; APPLICANT: Kasibhatla, Shailaja
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Tseng, Ben
; APPLICANT: Jessen, Katayoun Alavi
; APPLICANT: English, Nicole Marion
; APPLICANT: Maliartchouk, Serguei
; APPLICANT: Jiang, Songchun
; APPLICANT: Sirisoma, Nilantha Sudath
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Kuemmerle, Jared
; APPLICANT: Cytovia, Inc.
; TITLE OF INVENTION: Methods of Treating Diseases Responsive to Induction of Apoptosis
; FILE REFERENCE: 1735.084PC02
; CURRENT APPLICATION NUMBER: PCT/US04/11915
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/484,750
; PRIOR FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: US 60/463,649
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: US 60/532,665
; PRIOR FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: US 60/463,662
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: US 60/484,749
; PRIOR FILING DATE: 2003-07-07
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
PCT-US04-11915-41

Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
Db 1 DEVD 4

RESULT 3
PCT-US04-11916-23
; Sequence 23, Application PC/TUS0411916
; GENERAL INFORMATION:
; APPLICANT: Kasibhatla, Shailaja
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Tseng, Ben
; APPLICANT: Jessen, Katayoun Alavi
; APPLICANT: Maliartchouk, Serguei
; APPLICANT: English, Nicole Marion
; APPLICANT: Kuemmerle, Jared
; APPLICANT: Kemnitzner, William E.
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Kuemmerle, Jared
; APPLICANT: Cytovia, Inc.
; TITLE OF INVENTION: Methods of Treating Diseases Responsive to Induction of Apoptosis
; FILE REFERENCE: 1735.087PC01
; CURRENT APPLICATION NUMBER: PCT/US04/11916
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: 60/463,687
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT

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; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
PCT-US04-11916-23

Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
Db 1 DEVD 4

RESULT 4
US-10-768-976-64
; Sequence 64, Application US/10768976
; GENERAL INFORMATION:
; APPLICANT: Wood, Keith V.
; APPLICANT: Los, Georgyi V.
; APPLICANT: Bulleit, Robert F.
; APPLICANT: Klauber, Dieter
; APPLICANT: McDougall, Mark
; APPLICANT: Zimprich, Chad
; APPLICANT: Promega Corporation
; TITLE OF INVENTION: Covalent Tethering of Functional Groups to Proteins
; FILE REFERENCE: 341.020J51
; CURRENT APPLICATION NUMBER: US/10/768,976
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: US 60/444,094
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 60/474,659
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A synthetic peptide
US-10-768-976-64

Query Match 100.0%; Score 21; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
Db 1 DEVD 4

RESULT 5
US-10-630-926-14
; Sequence 14, Application US/10630926
; GENERAL INFORMATION:
; APPLICANT: Riccardi, Carlo
; TITLE OF INVENTION: INTRACELLULAR MODULATORS OF APOPTIC CELL
; DEATH PATHWAYS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEWMARK, P.L.L.C.
; STREET: 624 Ninth Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/10/630,926
FILING DATE: 31-Jul-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/403,861A
FILING DATE: 11-Feb-2000
APPLICATION NUMBER: PCT/EP98/02490
FILING DATE: 27-Apr-1998
APPLICATION NUMBER: EP 97107033.9
FILING DATE: 28-Apr-1997
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: RICCARDI=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: /note= "the N-terminus is modified by an acetyl group; the C-terminus is modified with a-(4-methyl-coumaryl-7-amide)"
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-630-926-14

Query Match 100.0%; Score 21; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
Db 1 DEVD 4

RESULT 6
US-10-626-905-43
GENERAL INFORMATION:
APPLICANT: FRANZOSO, GUIDO
APPLICANT: DESMAELE, ENRICO
APPLICANT: ZAZZERONI, FRANCESCA
APPLICANT: FAPA, SALVATORE
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING APOPTOSIS
FILE REFERENCE: 21459-94575
CURRENT APPLICATION NUMBER: US/10/626,905
CURRENT FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: PCT/US02/31548
PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: 10/263,330
PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: 60/328,811
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/326,492
PRIOR FILING DATE: 2001-10-02
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 43
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-626-905-43

Query Match 100.0%; Score 21; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
Db 1 DEVD 4
RESULT 7
US-10-626-258-22
GENERAL INFORMATION:
SEQUENCE 22, Application US/10626258
APPLICANT: Snively, Marshall
APPLICANT: Klionsky, Lana
TITLE OF INVENTION: Enhanced Solubility of Recombinant Proteins
FILE REFERENCE: A-725
CURRENT APPLICATION NUMBER: US/10/626,258
CURRENT FILING DATE: 2003-07-23
PRIOR APPLICATION NUMBER: US/09/715,521C
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.0
SEQ ID NO 22
LENGTH: 4
TYPE: PRT
ORGANISM: caspase 3 protease
US-10-626-258-22

Query Match 100.0%; Score 21; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
Db 1 DEVD 4

RESULT 8
US-10-471-720-1
GENERAL INFORMATION:
SEQUENCE 1, Application US/10471720
APPLICANT: Cai, Sui Xiong
APPLICANT: Reddy, P. Sanjeeva
APPLICANT: Drewe, John A.
APPLICANT: Nguyen, Bao Ngoc
APPLICANT: Kasibhatla, Shailaja
TITLE OF INVENTION: Multifluoro-substituted Chalcones and Analogs as Activators of Apoptosis and Inducers of Apoptosis and the Use Thereof
FILE REFERENCE: 1735.0540001
CURRENT APPLICATION NUMBER: US/10/471,720
CURRENT FILING DATE: 2003-09-15
PRIOR APPLICATION NUMBER: PCT/US02/07569
PRIOR FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: US 60/275,473
PRIOR FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fluorogenic substrate
US-10-471-720-1

Query Match 100.0%; Score 21; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
Db 1 DEVD 4

RESULT 9
US-10-030-378-1

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; Sequence 1, Application US/10030378
; GENERAL INFORMATION:
; APPLICANT: Blue, Jeffrey T.
; TITLE OF INVENTION: DETECTION OF VIRAL STABILITY
; FILE REFERENCE: 20455P
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/US00/12638
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 60/134,163
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: caspase 3 substrate
US-10-030-378-1

Query Match 100.0%; Score 21; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
Db 1 DEVD 4

RESULT 10
US-10-263-330A-43
; Sequence 43, Application US/10263330A
; GENERAL INFORMATION:
; APPLICANT: FRANZOSO, GUIDO
; APPLICANT: DESMAELE, ENRICO
; APPLICANT: ZAZZERONI, FRANCESCA
; APPLICANT: PAPA, SALVATORE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING APOPTOSIS
; FILE REFERENCE: 21459-93823
; CURRENT APPLICATION NUMBER: US/10/263,330A
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/328,811
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/326,492
; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patent in Ver. 3.2
; SEQ ID NO 43
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-263-330A-43

Query Match 100.0%; Score 21; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
Db 1 DEVD 4

RESULT 11
US-10-146-136-1
; Sequence 1, Application US/10146136
; GENERAL INFORMATION:
; APPLICANT: CAI, SUI XIONG
; APPLICANT: ZHANG, HONG
; APPLICANT: KENNITZER, WILLIAM
; Sequence 1, Application US/10816893
; GENERAL INFORMATION:
; APPLICANT: JIANG, SONGCHUN
; APPLICANT: DREWE, JOHN A.
; APPLICANT: STORER, RICHARD
; TITLE OF INVENTION: SUBSTITUTED COUMARINS AND QUINOLINES AND ANALOGS AS ACTIVATORS OF
; TITLE OF INVENTION: CASPASES AND INDUCERS OF APOPTOSIS AND THE USE THEREOF
; FILE REFERENCE: 1735.0660001
; CURRENT APPLICATION NUMBER: US/10/146,136
; CURRENT FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/290,978
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fluorogenic substrate
US-10-146-136-1

Query Match 100.0%; Score 21; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
Db 1 DEVD 4

RESULT 12
US-10-626-905A-43
; Sequence 43, Application US/10626905A
; GENERAL INFORMATION:
; APPLICANT: FRANZOSO, GUIDO
; APPLICANT: DESMAELE, ENRICO
; APPLICANT: ZAZZERONI, FRANCESCA
; APPLICANT: PAPA, SALVATORE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING APOPTOSIS
; FILE REFERENCE: 21459-94575
; CURRENT APPLICATION NUMBER: US/10/626,905A
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: PCT/US02/31548
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 10/263,330
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/328,811
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/326,492
; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patent in Ver. 3.2
; SEQ ID NO 43
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-626-905A-43

Query Match 100.0%; Score 21; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
Db 1 DEVD 4

RESULT 13
US-10-816-893-1
; Sequence 1, Application US/10816893
; GENERAL INFORMATION:
```

```
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Kasibhatla, Shailaja
; APPLICANT: Drewe, John
; APPLICANT: Reddy, P. Sanjeeva
; APPLICANT: Zhang, Han-zhong
; TITLE OF INVENTION: Substituted N'-(Arylcabonyl)-Benzhydrazides,
; TITLE OF INVENTION: N'-(Arylcabonyl)-Benzylidene-hydrazides And Analogs as Activators
; TITLE OF INVENTION: Caspases and Inducers of Apoptosis And The Use Thereof
; FILE REFERENCE: 1735.0360002
; CURRENT APPLICATION NUMBER: US/10/816,893
; CURRENT FILING DATE: 2004-04-05
; PRIOR APPLICATION NUMBER: US 10/141,769
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/289,803
; PRIOR FILING DATE: 2001-05-10
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fluorogenic substrate
; US-10-816-893-1

Query Match      100.0%; Score 21; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DEVD 4
      ||||
DB      1 DEVD 4

RESULT 15
US-10-826-923-23
; Sequence 23, Application US/10826923
; GENERAL INFORMATION:
; APPLICANT: Kasibhatla, Shailaja
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Tseng, Ben
; APPLICANT: Jessen, Katayoun Alavi
; APPLICANT: Maliartchouk, Serguei
; APPLICANT: English, Nicole Marion
; APPLICANT: Kuemmerle, Jared
; APPLICANT: Kennitzer, William E.
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Kuemmerle, Jared
; TITLE OF INVENTION: Methods of Treating Diseases Responsive to Induction of Apoptosis
; TITLE OF INVENTION: and Screening Assays
; FILE REFERENCE: 1735.0870001
; CURRENT APPLICATION NUMBER: US/10/826,923
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: 60/463,687
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; US-10-826-923-23

Query Match      100.0%; Score 21; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DEVD 4
      ||||
DB      1 DEVD 4

Search completed: May 24, 2004, 14:48:20
Job time : 13.5 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 24, 2004, 14:36:18 ; Search time 13.5 Seconds
(without alignments)
28,501 Million cell updates/sec

Title: US-09-765-105A-2

Perfect score: 21
Sequence: 1 DEVD 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 78: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	21	100.0	16	2	PL0137	protein kinase, 80
2	21	100.0	18	2	B34473	calcium-binding pr
3	21	100.0	44	2	B43714	hydroxymethylgluta
4	21	100.0	45	2	D95155	hypothetical prote
5	21	100.0	49	2	T21746	hypothetical prote
6	21	100.0	58	2	PQ0129	34.5K linker prote
7	21	100.0	60	2	C69169	hypothetical prote
8	21	100.0	67	2	T17388	vli protein - Dic
9	21	100.0	68	2	B71880	4-oxalocrotonate t
10	21	100.0	68	2	D64635	4-oxalocrotonate t
11	21	100.0	69	2	H81078	4-oxalocrotonate t
12	21	100.0	74	2	S82829	hypothetical prote
13	21	100.0	75	2	F64032	hypothetical prote
14	21	100.0	76	2	D91267	hypothetical prote
15	21	100.0	76	2	A86108	hypothetical prote
16	21	100.0	76	2	S56355	hypothetical 8.6K
17	21	100.0	82	2	A43337	sm region ORF1 pr
18	21	100.0	86	2	F70966	probable phage pro
19	21	100.0	97	2	E64509	hypothetical prote
20	21	100.0	98	1	W7WL11	E7 protein - human
21	21	100.0	98	1	W7WL6	E7 protein - human
22	21	100.0	98	1	W7WLC1	E7 protein - pygmy
23	21	100.0	99	2	E95237	preprotein translo
24	21	100.0	99	2	F98101	conserved hypothet
25	21	100.0	101	1	W7WL13	E7 protein - human
26	21	100.0	101	1	W7WL51	E7 protein - human
27	21	100.0	101	2	B86645	Glu-tRNA amidotran
28	21	100.0	103	2	F97138	hypothetical prote
29	21	100.0	104	2	A83871	hypothetical prote

30 21 100.0 105 2 F71348 probable DNA-bind
31 21 100.0 105 2 S06985 probable nitrogen
32 21 100.0 105 2 S36580 E7 protein - human
33 21 100.0 105 2 S36528 E7 protein - human
34 21 100.0 105 2 S36504 E7 protein - human
35 21 100.0 107 2 G72868 hypothetical prote
36 21 100.0 109 2 AD3826 hypothetical prote
37 21 100.0 110 2 H72774 hypothetical prote
38 21 100.0 110 2 S74013 hypothetical prote
39 21 100.0 112 2 H69372 hypothetical prote
40 21 100.0 112 2 F69320 conserved hypothet
41 21 100.0 113 1 W7WLR1 E7 protein - thesu
42 21 100.0 113 2 T13827 hypothetical prote
43 21 100.0 118 2 D84918 hypothetical prote
44 21 100.0 119 2 S17123 phage shock protei
45 21 100.0 119 2 C90864 phage shock protei

ALIGNMENTS

RESULT 1

PL0137
Protein Kinase, 80K - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 18-Jun-1993
C:Accession: PL0137
R:Decheret, J.; Weber, M.; Weber-Schaeuffelen, M.; Wollny, E.
J. Neurochem. 53, 1268-1275, 1989
A:Title: Isolation and partial characterization of an 80,000-dalton protein kinase fr
A:Reference number: PL0137; MUID:89361455; PMID:2769266
A:Accession: PL0137
A:Molecule type: Protein
A:Residues: 1-16 <DEC>
C:Comment: This protein has a novel serine/threonine-specific protein kinase activity.

Query Match 100.0%; Score 21; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
Db 2 DEVD 5

RESULT 2

B34473
Calcium-binding protein 4 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 31-Oct-1997
C:Accession: B34473
R:Van, P.N.; Peter, F.; Soeling, H.D.
J. Biol. Chem. 264, 17494-17501, 1989
A:Title: Four intracisternal calcium-binding glycoproteins from rat liver microsomes v
A:Reference number: A34473; MUID:90008920; PMID:2793869
A:Accession: B34473
A>Status: Preliminary
A:Molecule type: protein
A:Residues: 1-18 <VAN>
C:Superfamily: heat shock protein 90
C:Keywords: calcium binding

Query Match 100.0%; Score 21; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
Db 2 DEVD 5

RESULT 3

B43714
 hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) - Pseudomonas sp. (fragment)
 C:Species: Pseudomonas sp.
 C>Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 26-May-2000
 C/Accession: B43714
 R:Anderson, D.H.; Rodwell, V.W.
 J. Bacteriol. 171, 6468-6472, 1989
 A:Title: Nucleotide sequence and expression in *Escherichia coli* of the 3-hydroxy-3-methylglutaryl-CoA reductase (NADPH)
 A:Reference number: A43714; MUID:90078086; PMID:2687236
 A:Accession: B43714
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-44 <AND>
 A:Cross-references: GB:M31807; NID:G151370; PIDN:AAA25894.1; PID:G151371
 C:Superfamily: Methanococcus jannaschii hydroxymethylglutaryl-CoA reductase (NADPH)
 C:Keywords: coenzyme A; oxidoreductase

Query Match 100.0%; Score 21; DB 2; Length 44;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0

QY 1 DEVD 4
 ||||
 Db 14 DEVD 17

RESULT 4
 D95155
 hypothetical protein SPI339 [imported] - Streptococcus pneumoniae (strain TIGR4)
 C:Species: Streptococcus pneumoniae
 C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
 C/Accession: D95155
 R:Tetterlin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
 on, J.D.; Umayam, L.A.; White, C.; Salzberg, S.L.; Lewis, M.R.; Kadane, D.; Holtzapfel,
 nson, T.; Hickey, E.K.; Holt, I.E.
 Science 293, 498-506, 2001
 A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
 A:Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.
 A:Reference number: A95000; MUID:21357209; PMID:11463916
 A:Accession: D95155
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-45 <KUR>
 A:Cross-references: GB:AE005672; PIDN:AAK75437.1; PID:G14972822; GSPDB:GN00164; TIGR:SP4
 A:Experimental source: strain TIGR4
 C:Genetics:
 A:Gene: SPI339

Query Match 100.0%; Score 21; DB 2; Length 45;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0

QY 1 DEVD 4
 ||||
 Db 19 DEVD 22

RESULT 5
 T21746
 hypothetical protein F35C12.1 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C/Accession: T21746
 R:Baynes, C.
 submitted to the EMBL Data Library, October 1996
 A:Reference number: Z19468
 A:Accession: T21746
 A>Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-49 <WIL>
 A:Cross-references: EMBL:Z81075; PIDN:CAB03046.1; GSPDB:GN00019; CESP:F35C12.1
 A:Experimental source: Clone F35C12
 C:Genetics:

A:Gene: CESP:F35C12.1
 A:Map position: 1
 A:Introns: 15/2

Query Match 100.0%; Score 21; DB 2; Length 49;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0

QY 1 DEVD 4
 ||||
 Db 33 DEVD 36

RESULT 6
 PQ0129
 34.5K linker protein - *Fischerella* sp. (fragment)
 C:Species: *Fischerella* sp.
 C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-Jan-2000
 C/Accession: PQ0129
 R:Eberlein, M.; Kufer, W.
 Gene 94, 133-136, 1990
 A:Title: Genes encoding both subunits of phycoerythrocyanin, a light-harvesting biliprotein
 A:Reference number: JQ0763; MUID:91033055; PMID:2121619
 A:Accession: PQ0129
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-58 <EBE>
 A:Cross-references: GB:M34254
 C:Superfamily: phycocyanin linker protein cpcH3

Query Match 100.0%; Score 21; DB 2; Length 58;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0

QY 1 DEVD 4
 ||||
 Db 13 DEVD 16

RESULT 7
 C69169
 hypothetical protein MTH525 - *Methanobacterium thermoautotrophicum* (strain Delta H)
 C:Species: *Methanobacterium thermoautotrophicum*
 C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
 C/Accession: C69169
 R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
 ki, S.; Church, G.M.; Daniels, C.J.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N
 J. Bacteriol. 179, 7135-7155, 1997
 A:Title: Complete genome sequence of *Methanobacterium thermoautotrophicum* Delta H: func
 A:Reference number: A69000; MUID:98037514; PMID:9371463
 A:Accession: C69169
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-60 <MTH>
 A:Cross-references: GB:AE000835; GB:AE000666; NID:G2621586; PIDN:AAB85031.1; PID:G26215
 A:Experimental source: strain Delta H
 C:Genetics:
 A:Gene: MTH525

Query Match 100.0%; Score 21; DB 2; Length 60;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0

QY 1 DEVD 4
 ||||
 Db 22 DEVD 25

RESULT 8
 T17388
 vrr1 protein - *Dichelobacter nodosus*
 C:Species: *Dichelobacter nodosus*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T17388
R;Billington, S.J.; Huggins, A.S.; Johansen, P.A.; Crellin, P.K.; Chung, J.K.; Katz, M
Infect. Immun. 67, 1277-1286, 1999
A;Title: Complete nucleotide sequence of the 27-kilobase virulence related locus (vrl) o
A;Reference number: Z18734; MUID:99150261; PMID:10024571
A;Accession: T17388
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-67 <BL>
A;Cross-references: EMBL:U20246; NID:G3493323; PID:G3482870; PIDN:AAC33397.1
A;Experimental source: strain A198

Query Match 100.0%; Score 21; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 2.6e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

QY 1 DEVD 4
|||
45 DEVD 48

Db

RESULT 9
B71880
4-oxalocrotonate tautomerase (EC 5.3.2.-) jhp0858 [similarity] - Helicobacter pylori (st
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 17-Mar-2000
C;Accession: B71880
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: B71880
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-68 <ARN>
A;Cross-references: GB:AE001515; GB:AE001439; NID:G4155425; PIDN:AAD06434.1; PID:G415542
A;Experimental source: strain J99
C;Genetics:
A;Gene: jhp0858
C;Superfamily: 4-oxalocrotonate tautomerase
C;Keywords: aromatic hydrocarbon catabolism; intramolecular oxidoreductase; isomerase
F;2-68/Product: 4-oxalocrotonate tautomerase #status predicted <MAT>
F;2/Active site: Pro #status predicted

Query Match 100.0%; Score 21; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 2.6e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

QY 1 DEVD 4
|||
47 DEVD 50

Db

RESULT 10
D64635
4-oxalocrotonate tautomerase (EC 5.3.2.-) HP0924 [similarity] - Helicobacter pylori (str
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 17-Mar-2000
C;Accession: D64635
R;Tomb, J.F.; White, O.; Karlavags, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khairak, H.G.; Glodek, A.; McKenna
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: D64635
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-68 <TOW>

A;Cross-references: GB:AE000602; GB:AE000511; NID:G2314060; PIDN:AAD07977.1; PID:G2314
C;Superfamily: 4-oxalocrotonate tautomerase
C;Keywords: aromatic hydrocarbon catabolism; intramolecular oxidoreductase; isomerase
F;2-66/Product: 4-oxalocrotonate tautomerase #status predicted <MAT>
F;2/Active site: Pro #status predicted

Query Match 100.0%; Score 21; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 2.6e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

QY 1 DEVD 4
|||
47 DEVD 50

Db

RESULT 11
H81078
4-oxalocrotonate tautomerase (EC 5.3.2.-) NMB1474 [similarity] - Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Feb-2001
C;Accession: H81078; H81863
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, C.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizzi, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: H81078
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-69 <TET>
A;Cross-references: GB:AE002497; GB:AE002098; NID:G7226712; PIDN:AAF41831.1; PID:G7226
A;Experimental source: serogroup B, strain MC58
R;Parthill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; McI
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandrea
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: H81863
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-69 <PAR>
A;Cross-references: GB:AL162756; GB:AL157959; NID:G7380091; PIDN:CAE84913.1; PID:G7380
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMB1474; NMA1685
C;Superfamily: 4-oxalocrotonate tautomerase
C;Keywords: aromatic hydrocarbon catabolism; intramolecular oxidoreductase; isomerase
F;2-69/Product: 4-oxalocrotonate tautomerase #status predicted <MAT>
F;2/Active site: Pro #status predicted

Query Match 100.0%; Score 21; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 2.7e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

QY 1 DEVD 4
|||
47 DEVD 50

Db

RESULT 12
E82829
hypothetical protein XF0242 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: E82829
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: E82829

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-74 <SIN>
A;Cross-references: GB:AE003878; GB:AE003849; NID:g9105052; PIDN:AAF83055.1; GSPDB:GN00154
A;Experimental source: strain 9a5C
A;Experimental sources: strain 9a5C
R;Simpton, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, P.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Camargo, D.M.; Carrer, H. as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira M.; Tsuchiko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF0242

Query Match 100.0%; Score 21; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
    ||||
Db 64 DEVD 67

RESULT 13
F64032
hypothetical protein H1497 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
C;Accession: F64032
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kervlavage, A.; Gocayne, J.D.; Scott, J.; Shiley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: F64032
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-75 <TIGR>
A;Cross-references: GB:U32826; GB:L42023; NID:g1574322; PIDN:AAC23137.1; PID:g1574327; T

Query Match 100.0%; Score 21; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
    ||||
Db 31 DEVD 34

RESULT 14
D91267
hypothetical protein ECs5108 [imported] - Escherichia coli (strain O157:H7, substrain R1
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: D91267
R;Hayaishi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene A;Reference number: A95629; MUID:21156231; PMID:11258796
A;Accession: D91267
A;Status: preliminary
A;Molecule type: DNA
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A;Residues: 1-76 <HAY>
A;Cross-references: GB:BA000007; PIDN:BA83851.1; PID:g13364585; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain R1MD 050952
C;Genetics:
A;Gene: ECs5108

Query Match 100.0%; Score 21; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
    ||||
Db 52 DEVD 55

RESULT 15
A86108
hypothetical protein yjdi [imported] - Escherichia coli (strain O157:H7, substrain EDL5
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: A86108
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhiller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A86108
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-76 <STO>
A;Cross-references: GB:AE005174; NID:g12519102; PIDN:AAG59325.1; GSPDB:GN00145; UWGP:Z:
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: yjdi

Query Match 100.0%; Score 21; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
    ||||
Db 52 DEVD 55

Search completed: May 24, 2004, 14:41:40
Job time : 14.5 secs
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OM protein - protein search, using sw model

Run on: May 24, 2004, 14:36:17 ; Search time 10.5 Seconds
(without alignments)
19.836 Million cell updates/sec

Title: US-09-765-105A-2

Perfect score: 21
Sequence: 1 DEVD 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	21	100.0	20	1 FIBB_SHEEP	P14470 ovis aries
2	21	100.0	21	1 FIBB_ODOHE	P14476 odocoileus
3	21	100.0	60	1 YC60_BRAJA	Q89429 bradyrhizob
4	21	100.0	63	1 MIP_BOTAS	P10077 bothrops as
5	21	100.0	67	1 Y858_HELPF	Q92857 helicobacte
6	21	100.0	67	1 Y924_HELPF	O25581 helicobacte
7	21	100.0	75	1 YE97_HAEIN	P44221 haemophilus
8	21	100.0	76	1 YJDI_ECOLI	P39273 escherichia
9	21	100.0	77	1 MP5A_AMBPS	P43174 ambrosia ps
10	21	100.0	88	1 EF1B_TREAC	Q9hkl1 thermoplas
11	21	100.0	95	1 LSM2_HUMAN	Q9y333 homo sapien
12	21	100.0	97	1 VE7_HPV44	Q80914 human papil
13	21	100.0	97	1 VE7_HPV55	Q80935 human papil
14	21	100.0	97	1 YG75_METJA	Q59073 methanococ
15	21	100.0	98	1 VE7_HPV11	P04020 human papil
16	21	100.0	98	1 VE7_HPV6A	Q84292 human papil
17	21	100.0	98	1 VE7_HPV6B	P06464 human papil
18	21	100.0	98	1 VE7_PCFV1	Q02272 pygmy chimp
19	21	100.0	101	1 GATC_LACLA	Q9CJ44 lactococcus
20	21	100.0	101	1 VE7_HPV13	Q02271 human papil
21	21	100.0	101	1 VE7_HPV51	P26558 human papil
22	21	100.0	105	1 DBH_TREPA	O83278 treponema p
23	21	100.0	105	1 GLMT_METTL	P35771 methanococ
24	21	100.0	105	1 VE7_HPV30	P36826 human papil
25	21	100.0	105	1 VE7_HPV53	P36832 human papil
26	21	100.0	105	1 VE7_HPV56	P36833 human papil
27	21	100.0	113	1 CYAY_RALSO	Q8XV54 raietonia s
28	21	100.0	113	1 VE7_RHPV1	P22161 rhesus papil
29	21	100.0	119	1 PSPC_ECOLI	P23855 escherichia
30	21	100.0	129	1 YSXI_CAREL	Q10020 caenorhabdi
31	21	100.0	133	1 ATPE_MYCGE	P47638 mycoplasma
32	21	100.0	135	1 RS6E_HALMA	P21509 halocarcia
33	21	100.0	138	1 YFFO_ECOLI	P76546 escherichia

34	21	100.0	140	1 BSR_BACCE	P33967 bacillus ce
35	21	100.0	147	1 CALM_FRAGS	Q39752 fagus sylv
36	21	100.0	148	1 CALM_EMENI	P19533 emericella
37	21	100.0	148	1 CALM_MAGGR	Q9uwi0 magnaporthe
38	21	100.0	148	1 CALM_NEUCR	Q02052 neurospora
39	21	100.0	148	1 CALM_PARTE	P07463 paramecium
40	21	100.0	151	1 DKSA_ECOLI	P18274 escherichia
41	21	100.0	151	1 DKSA_SALTY	Q9ziw3 salmonella
42	21	100.0	151	1 TPC2_BALNU	P21798 balanus nub
43	21	100.0	151	1 YD97_THETN	Q8ra33 thermoaer
44	21	100.0	151	1 YKA2_YEAST	P36108 saccharomyc
45	21	100.0	152	1 Y534_BRUME	Q8yib0 brucella me

ALIGNMENTS

RESULT 1

FIBB_SHEEP
ID FIBB_SHEEP STANDARD; PRT; 20 AA.
AC P14470;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Ovis aries (Sheep), and
OC Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940, 9925;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 13:1789-1791(1965).
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
polymerize into fibrin and acting as a cofactor in platelet
aggregation.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
(ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
which cleaves fibrinopeptides A and B from alpha and beta chains,
and thus exposes the N-terminal polymerization sites responsible
for the formation of the soft clot.
DR InterPro: IPR002181; Fibrinogen_C.
DR PROSITE: PS00514; FIBRIN AG C DOMAIN; PARTIAL.
KW Blood coagulation; Plasma; Sulfation.
FT PEPTIDE 1 20 FIBRINOPEPTIDE B.
FT MOD_RES 5 20 SULFATION.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2338 MW; FCF5B6FF0DEC6627 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 44;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4

DB 6 DEVD 9

RESULT 2

FIBB_ODOHE
ID FIBB_ODOHE STANDARD; PRT; 21 AA.
AC P14476;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).

GN FGB.

OS Odocoileus hemionus (Mule deer) (Black-tailed deer).

CC Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
CC Cervidae; Odocoileinae; Odocoileus.
CX NCBI_TaxID=9872;
RN [1]
RP SEQUENCE.
RX MEDLINE=67209145; PubMed=6033721;
RA Doolittle R.F., Schubert D., Schwartz S.A.; fibrinopeptides. I.
RT "Amino acid sequence studies on arriodactyl fibrinopeptides. I.
RT Dromedary camel, mule deer, and cape buffalo.";
RL Arch. Biochem. Biophys. 118:456-467(1967).
CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
DR InterPro: IPR002181; Fibrinogen C.
DR PROSITE: PS00514; FIBRIN_AG_C DOMAIN; PARTIAL.
KW Blood coagulation; Plasma; Sulfation; Pyrrolidone carboxylic acid.
FT PEPTIDE 1 21 FIBRINOPEPTIDE B.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON TER 6 6 SULFATION.
SQ SEQUENCE 21 AA; 2496 MW; FCF562C51A0C1627 CRC64;
Query Match 100.0%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DEVD 4
DB 7 DEVD 10
RESULT 3
YC60 BRAJA STANDARD; PRT; 60 AA.
ID Q89U29;
AC 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical zinc-binding UPF0243 protein bsr1260.
GN BSR1260.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=USDA 110;
RA Kaneo T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idegawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
CC -1- COFACTOR: Binds 1 zinc ion (By similarity).
CC -1- SIMILARITY: Belongs to the UPF0243 family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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DR EMBL; AP005939; BAC46525.1; -.
DR HAMAP; MF_00649; -; 1.
DR InterPro: IPR005584; DUF329.
DR Pfam; PF03884; DUF329; 1.
KW Hypothetical protein; zinc; Metal-binding; Complete proteome.
FT METAL 15 15 ZINC (BY SIMILARITY).
FT METAL 18 18 ZINC (BY SIMILARITY).
FT METAL 30 30 ZINC (BY SIMILARITY).
FT METAL 34 34 ZINC (BY SIMILARITY).
SQ SEQUENCE 60 AA; 6692 MW; C7DSFFFE0278BD9 CRC64;
Query Match 100.0%; Score 21; DB 1; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DEVD 4
DB 54 DEVD 57
RESULT 4
MIP BOTAS STANDARD; PRT; 63 AA.
ID MIP BOTAS
AC P81077;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Myotoxin inhibitor protein MIP.
OS Bothrops asper (Terciopelo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8722;
RN [1]
RP SEQUENCE.
RC TISSUE=Blood;
RX MEDLINE=97439729; PubMed=9307037;
RA Lizano S., Lomonte B., Fox J.W., Gutierrez J.M.;
RT "Biochemical characterization and pharmacological properties of a
RT phospholipase A2 myotoxin inhibitor from the plasma of the snake
RT Bothrops asper.";
RL Biochem. J. 326:853-859(1997).
CC -1- FUNCTION: Binds to and neutralizes the activities of basic
CC phospholipase A2 (PLA2) myotoxin isoforms.
CC -1- SUBUNIT: Oligomer composed of five 23-25 kDa subunits.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
KW Glycoprotein; Plasma; Lectin.
SQ SEQUENCE 63 AA; 7154 MW; F1E6AF75D8489CE6 CRC64;
Query Match 100.0%; Score 21; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DEVD 4
DB 1 DEVD 4
RESULT 5
Y858 HELPJ STANDARD; PRT; 67 AA.
ID Y858 HELPJ
AC Q9ZK37;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable tautomerase JHP0858 (EC 5.3.2.-).
GN JHP0858.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN [1]

```

RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown B.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
CC -!- SIMILARITY: Belongs to the tautomerase family.
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CC -----
DR EMBL; AE001515; AAD06434.1; -.
DR PIR; B71880; B71880.
DR HAMAP; MF 00718; -.
DR InterPro; IPR004370; Taut.
DR Pfam; PF01361; Tautomerase; 1.
DR ProDom; PD404143; Taut; 1.
DR TIGRFAMS; TIGR00013; Taut; 1.
KW Isomerase; Complete proteome.
FT INIT MET 0
FT ACT SITE 1 1 CATALYTIC BASE (BY SIMILARITY).
FT SEQUENCE 67 AA; 7394 MW; F5AD98AA31A73BFB CRC64;
SQ SEQUENCE 67 AA; 7394 MW; F5AD98AA31A73BFB CRC64;

Query Match 100.0%; Score 21; DB 1; Length 67;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
DB 46 DEVD 49

RESULT 6
Y924_HELPY
ID Y924_HELPY STANDARD; PRT; 67 AA.
AC Q25581;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable tautomerase HP0924 (EC 5.3.2.-).
GN HP0924.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=26695 / ATCC 700992;
RX MEDLINE=9739467; PubMed=9252185;
RA Tomb J.-F., White O., Kervage A.R., Clayton R.A., Sutton G.G., B.A.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty S.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori.";
RL Nature 388:539-547(1997).
CC -!- SIMILARITY: Belongs to the tautomerase family.
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CC -----
DR EMBL; AE000602; AAD07977.1; -.
DR PIR; D64635; D64635.
DR TIGR; HP0924; -.
DR HAMAP; MF 00718; -.
DR InterPro; IPR004370; Taut.
DR Pfam; PF01361; Tautomerase; 1.
DR ProDom; PD404143; Taut; 1.
DR TIGRFAMS; TIGR00013; Taut; 1.
KW Isomerase; Complete proteome.
FT INIT MET 0
FT ACT SITE 1 1 CATALYTIC BASE (BY SIMILARITY).
FT SEQUENCE 67 AA; 7380 MW; 36AD98AA31A73EE9 CRC64;
SQ SEQUENCE 67 AA; 7380 MW; 36AD98AA31A73EE9 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 67;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
DB 46 DEVD 49

RESULT 7
YE97_HAEIN
ID YE97_HAEIN STANDARD; PRT; 75 AA.
AC P44221;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein H1497.
GN H1497.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kervage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzgugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
CC -!- SIMILARITY: Contains 1 dksA/trar-type zinc finger.
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CC -----
DR EMBL; U32826; AAC23137.1; -.
DR PIR; F64032; F64032.
DR TIGR; H1497; -.
DR InterPro; IPR000962; Znf_dksA_Trar.
DR Pfam; PF01258; zf_dksA_trar; 1.

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```
DR PRINTS; PR00618; DKSZNFINGER.
DR PROSITE; PS01102; DKSATRR_ZN_FINGER; 1.
KW Hypothetical protein; Zinc-finger; Complete proteome.
SQ ZN FING 43 67 TSAR/DKSA-TYPE.
SQ SEQUENCE 75 AA; 8405 MW; 9F6DAD6F2C02C626 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 75;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
Db 31 DEVD 34

RESULT 8
YDJI_ECOLI STANDARD; PRT; 76 AA.
AC P39273;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein ydji.
GN YDJI OR B4146 OR B5728 OR ECS5108.
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MGL655;
RX MEDLINE=95334362; PubMed=7610040;
RA Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
RA Blattner F.R.;
RT "Analysis of the Escherichia coli genome VI: DNA sequence of the
RL Nucleic Acids Res. 23:2105-2119(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.C., Davis N.W., Lim A., Dimalanta E.F., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RN Nature 409:529-533(2001).
RL [3]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RMD 0509952;
RX MEDLINE=21156231; PubMed=11558796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Toke T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RL O157:H7 and genomic comparison with a laboratory strain K-12.";
RN DNA Res. 8:11-22(2001).
CC -----
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CC -----
DR EMBL; U14003; AAA97026.1; -.
DR EMBL; AE000485; AAC70087.1; -.
DR EMBL; AE005646; AAG59325.1; -.

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DR EMBL; AP002568; BAB38531.1; -.
DR FIR; A86108; A86108.
DR FIR; D91267; D91267.
DR FIR; S56355; S56355.
DR EcoGene; EG12466; YJDI.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 76 AA; 8550 MW; 062C085C008C20AC CRC64;

Query Match 100.0%; Score 21; DB 1; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
Db 52 DEVD 55

RESULT 9
MP5A_AMBPS STANDARD; PRT; 77 AA.
AC P43174;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Pollen allergen Amb p 5a precursor (Amb p Va).
OS Ambrosia psilostachya (Western ragweed).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; asterids;
OC Campanulids; Asterales; Asteraceae; Asteroideae; Helianthaceae;
OC Ambrosia.
OX NCBI_TaxID=29715;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 23-63.
RC TISSUE=Pollen;
RX MEDLINE=94194048; PubMed=7511632;
RA Ghosh B., Rafnar T., Perry M.P., Bassolino-Klimas D.,
RA Mettler W.J., Klapper D.G., Marsh D.G.;
RT "Immunologic and molecular characterization of Amb p V allergens from
RL Ambrosia psilostachya (Western Ragweed) pollen.";
RJ J. Immunol. 152:2882-2889(1994).
CC -!- ALLERGEN: Causes an allergic reaction in human.
CC -----
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CC -----
DR EMBL; L24465; AAA20065.1; -.
DR EMBL; L24466; AAA20067.1; -.
DR HSSP; P10444; LBGG.
DR InterPro; IPR005611; Amb_V_allergen.
DR Pfam; PF03913; Amb_V_allergen; 1.
DR ProDom; PD018950; Amb_V_allergen; 1.
KW Allergen; Signal.
FT SIGNAL 1 22
FT CHAIN 23 77 POLLEN ALLERGEN AMB P 5A.
FT DISULFID 26 61 BY SIMILARITY.
FT DISULFID 33 48 BY SIMILARITY.
FT DISULFID 40 54 BY SIMILARITY.
FT DISULFID 41 65 BY SIMILARITY.
FT VARIANT 59 59 E -> K (IN CLONE A3).
SQ SEQUENCE 77 AA; 8710 MW; 2D8976EB65D9A00F CRC64;

Query Match 100.0%; Score 21; DB 1; Length 77;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
Db 15 DEVD 19

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RESULT 10
 EF1B_THEAC STANDARD; PRT; 88 AA.
 ID EF1B_THEAC
 AC Q9HKN1;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Elongation factor 1-beta (EF1-beta).
 GN EF1B OR TA0566.
 OS Thermoplasma acidophilum.
 OC Archaea; Euryarchaeota; Thermoplasmatia; Thermoplasmatiales;
 OC Thermoplasmataceae; Thermoplasma.
 OX NCBI_TaxID=2303;
 RN [1]_TaxID=2303;
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSM 1728;
 RX MEDLINE=20479972; PubMed=11029001;
 RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
 RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
 RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma
 RT acidophilum.";
 RL Nature 407:508-513 (2000).
 CC -!- FUNCTION: Promotes the exchange of GDP for GTP in EF-1-alpha/GDP,
 CC thus allowing the regeneration of EF-1-alpha/GTP that could then
 CC be used to form the ternary complex EF-1-alpha/GTP/AATRNA (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the EF-1-beta/EF-1-delta family.
 CC
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 CC
 CC
 DR EMBL; AL445064; CAC11706.1; ALT_INIT.
 DR HSP; O27734; IGH8.
 DR HAMAP; MF_00043; -; 1.
 DR InterPro; IPR004542; aEF-1_beta.
 DR InterPro; IPR001326; EF1_BD.
 DR Pfam; PF00736; EF1BD; 1_
 DR TIGRfam; TIGR00489; aEF1_beta; 1.
 KW Elongation factor; Protein biosynthesis; Complete proteome.
 SQ SEQUENCE 88 AA; 9749 MW; 572357C1BADE5DA7 CRC64;

 Query Match 100.0%; Score 21; DB 1; Length 88;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 DEVD 4
 DB 40 DEVD 43
 |||||

 RESULT 11
 LSM2_HUMAN STANDARD; PRT; 95 AA.
 ID LSM2_HUMAN
 AC Q9Y333;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE U5 snRNP-associated Sm-like protein LSM2 (Small nuclear ribonuclear
 DE protein D homolog) (G7b) (SnRNP core SM-like protein SM-x5).
 GN LSM2 OR C6ORF28 OR G7B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RX MEDLINE=99452783; PubMed=10523320;
 RA Acheel T., Brahms H., Kastner B., Bachi A., Wilm M., Luehrmann R.;
 RT "A doughnut-shaped heteromer of human Sm-like proteins binds to the
 RT 3'-end of U6 snRNA, thereby facilitating U4/U6 duplex formation in
 RT vitro.";
 RL EMBO J. 18:5789-5802 (1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Olavesen M.G., Campbell R.D.;
 RT "Characterisation of the novel gene G7b located in the class III
 RT region of the human major histocompatibility complex.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A.,
 RA Abbasi N., Dickhoff R., Loretz C., Madan A., Dors M., Young J.,
 RA Lasky S., Hood L.;
 RT "Sequence of the human major histocompatibility complex class III
 RT region.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Shiina S., Tamiya G., Oka A., Inoko H.;
 RT "Homo sapiens 21229,817bp genomic DNA of 6p21.3 HLA class I region.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hypothalamus;
 RX MEDLINE=20402571; PubMed=10931946;
 RA Hu R.-M., Han Z.-G., Song H.-D., Peng Y.-D., Huang Q.-H., Ren S.-X.,
 RA Gu Y.-J., Huang C.-H., Li Y.-B., Jiang C.-L., Fu G., Zhang Q.-H.,
 RA Gu B.-W., Dai M., Mao Y.-F., Gao G.-F., Rong R., Ye M., Zhou J.,
 RA Xu S.-H., Gu J., Shi J.-X., Jin W.-R., Zhang C.-K., Wu T.-M.,
 RA Huang G.-Y., Chen Z., Chen M.-D., Chen J.-L.;
 RT "Gene expression profiling in the human hypothalamus-pituitary-adrenal
 RT axis and full-length cDNA cloning.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:9543-9548 (2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Schwardt A., Presser F., Paulmichl M.;
 RT "Human SMX5 homolog.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Gasavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madao A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalski U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -!- FUNCTION: Binds specifically to the 3'-terminal U-tract of U6
 CC snRNA.
 CC -!- SUBUNIT: LSM subunits form a heteromer with a doughnut shape.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -!- SIMILARITY: Belongs to the snRNP Sm proteins family.
 CC
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DR EMBL; AF182288; AAD56226.1; -
DR EMBL; AJ245416; CAB52190.1; -
DR EMBL; AF134726; AAD21818.1; -
DR EMBL; AF000503; BAB63302.1; -
DR EMBL; AF136977; AAG49438.1; -
DR EMBL; AF196468; AAG33023.1; -
DR EMBL; BC009192; AAH09192.1; -
DR Genew; HGNC:13940; LSM2.
DR GK; Q9V333; -
DR MIM; 607282; -
DR GO; GO:0005634; C:nucleus; NAS.
DR GO; GO:0017070; F:U6 snRNA binding; NAS.
DR GO; GO:0000398; P:nuclear mRNA splicing, via spliceosome; NAS.
DR InterPro; IPR006649; snRNP.
DR InterPro; IPR001163; snRNP_Sm.
DR Pfam; PF01423; LSM; 1.
DR ProDom; PD020287; snRNP; 1.
DR SMART; SMO0651; Sm; 1.
DR Nuclear protein; Ribonucleoprotein; mRNA splicing; mRNA processing;
KW RNA-binding.
SQ SEQUENCE 95 AA; 10834 MW; 623591A09A6ABACE CRC64;

Query Match 100.0%; Score 21; DB 1; Length 95;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
Db 75 DEVD 78

RESULT 12
ID VE7_HPV44 STANDARD; PRT; 97 AA.
AC Q80314;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE E7 protein.
GN E7.
OS Human papillomavirus type 44.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10592;
RN [1]
RP SEQUENCE FROM N.A.
RA Delius H.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: E7 PROTEIN HAS BOTH TRANSFORMING AND TRANS-ACTIVATING
CC ACTIVITIES.
CC

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DR EMBL; U31791; AAA79479.1; -
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
DR Early protein; Transcription regulation; Oncogene;
KW DNA-binding; Trans-acting factor.
FT SITE 57 60 C-XX-C MOTIF-1.
FT SITE 90 93 C-XX-C MOTIF-2.

SQ SEQUENCE 97 AA; 10641 MW; E4866AE13E050456 CRC64;
Query Match 100.0%; Score 21; DB 1; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
Db 34 DEVD 37

RESULT 13
ID VE7_HPV55 STANDARD; PRT; 97 AA.
AC Q80935;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE E7 protein.
GN E7.
OS Human papillomavirus type 55.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=37114;
RN [1]
RP SEQUENCE FROM N.A.
RA Delius H.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: E7 PROTEIN HAS BOTH TRANSFORMING AND TRANS-ACTIVATING
CC ACTIVITIES.
CC

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DR EMBL; U31791; AAA79479.1; -
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
DR Early protein; Transcription regulation; Oncogene;
KW DNA-binding; Trans-acting factor.
FT SITE 57 60 C-XX-C MOTIF-1.
FT SITE 90 93 C-XX-C MOTIF-2.
SQ SEQUENCE 97 AA; 10621 MW; E2997616BCE47D42 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
Db 34 DEVD 37

RESULT 14
ID YG79_METJA STANDARD; PRT; 97 AA.
AC Q59073;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ1679.
GN MJ1679.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;


```

RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RL Science 273:1058-1073(1996).
CC -----
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CC -----
DR EMBL; U67607; AAB99704.1; -.
DR PIR; E64509; E64509.
DR TIGR; M01679; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 97 AA; 11880 MW; 64C59303B9101FE0 CRC64;
Query Match 100.0%; Score 21; DB 1; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DEVD 4
DB 82 DEVD 85
RESULT 15
VE7 HPV11 STANDARD; PRT; 98 AA.
ID P04020;
AC 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE E7 protein.
GN E7.
OS Human papillomavirus type 11.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
CC Papillomavirus.
CX NCBI_TaxID=10580;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86181601; PubMed=3008427;
RA Dartmann K., Schwarz E., Giesmann L., Zur Hausen H.;
RT "The nucleotide sequence and genome organization of human papilloma
RL virus type 11."
RL Virology 151:124-130(1986).
RN [2]
RP SEQUENCE FROM N.A.
RA Fife K.H., Fan L., Fritsch M.H., Bryan J., Brown D.R.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: E7 PROTEIN HAS BOTH TRANSFORMING AND TRANS-ACTIVATING
CC ACTIVITIES.
CC -!- SIMILARITY: LOCAL WITH ADENOVIRUS E1A AND SV40 LT.
CC -----
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CC -----
DR EMBL; M14119; AAA46928.1; -.

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DR EMBL; L36108; AAA21704.1; -.
DR PIR; A03690; W7KL11.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
KW Early protein; Transcription regulation; Oncogene;
KW DNA-binding; Trans-acting factor.
FT SITE 58 61 C-XX-C MOTIF-1.
FT SITE 91 94 C-XX-C MOTIF-2.
SQ SEQUENCE 98 AA; 10889 MW; AACAA9A60C933E1F6 CRC64;
Query Match 100.0%; Score 21; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DEVD 4
DB 35 DEVD 38
Search completed: May 24, 2004, 14:39:34
Job time : 11.5 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 24, 2004, 14:36:17 ; Search time 36.5 Seconds
(without alignments)
34.577 Million cell updates/sec

Title: US-09-765-105A-2

Perfect score: 21

Sequence: 1 DEVD 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	21	100.0	11	10	O82070
2	21	100.0	44	2	Q51913
3	21	100.0	45	10	O49798
4	21	100.0	45	16	O97087
5	21	100.0	45	16	O8FVL6
6	21	100.0	49	4	Q8EP95
7	21	100.0	49	5	Q9XVP5
8	21	100.0	50	11	Q63952
9	21	100.0	53	13	Q9IAB6
10	21	100.0	53	16	Q98IWB
11	21	100.0	54	9	Q38258
12	21	100.0	54	9	Q38280
13	21	100.0	54	10	Q84NR3
14	21	100.0	54	17	Q977A0
15	21	100.0	56	12	Q99H60
16	21	100.0	56	12	Q99H57

17 21 100.0 56 12 Q99H59
18 21 100.0 57 10 Q8LH38
19 21 100.0 57 16 Q8NPJ7
20 21 100.0 59 5 Q94755
21 21 100.0 60 2 Q93AL7
22 21 100.0 60 10 Q7XEA8
23 21 100.0 60 17 Q26625
24 21 100.0 62 16 Q98IK2
25 21 100.0 63 2 Q83XT1
26 21 100.0 63 17 Q8PTV7
27 21 100.0 65 2 Q83XT8
28 21 100.0 65 13 Q9PTR0
29 21 100.0 65 16 Q8FE2
30 21 100.0 66 10 Q42235
31 21 100.0 66 16 Q83AS5
32 21 100.0 67 2 Q86180
33 21 100.0 67 2 Q83XT3
34 21 100.0 67 12 Q8VAS6
35 21 100.0 68 16 Q8CMB4
36 21 100.0 69 2 Q83XT7
37 21 100.0 69 2 Q83XS7
38 21 100.0 69 16 Q9UR69
39 21 100.0 70 12 Q8VES0
40 21 100.0 70 12 Q7TDK9
41 21 100.0 70 16 Q9CJQ9
42 21 100.0 71 2 Q83XU0
43 21 100.0 71 2 Q83XT6
44 21 100.0 71 2 Q83XT2
45 21 100.0 71 2 Q83XS8

ALIGNMENTS

RESULT 1

O82070 PRELIMINARY; PRT; 11 AA.
ID O82070
AC O82070;
DC 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE RNA polymerase (EC 2.7.7.6) (Fragment).
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cnv. Chinese Spring;
RA Young D.A.; Allen R.; Harvey A.J.; Lonsdale D.M.;
RT "Characterization of a gene encoding a single-subunit RNA polymerase from maize which is alternatively spliced."
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ005344; CAA06489.1;
DR GO; GO:0003899; F:DNA-directed RNA polymerase activity; IEA.
DR GO; GO:0003900; F:DNA-directed RNA polymerase I activity; IEA.
DR GO; GO:0003901; F:DNA-directed RNA polymerase II activity; IEA.
DR GO; GO:0003902; F:DNA-directed RNA polymerase III activity; IEA.
KW Nucleotidyltransferase; Transferase.
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1329 MW; CD96344923240AB2 CRC64;

Query Match 100.0%; Score 21; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4

Db 2 DEVD 5

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RESULT 2
Q51913 ID Q51913 PRELIMINARY; PRT; 44 AA.
AC Q51913;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE HMG-CoA-reductase (Fragment).
OS Pseudomonas mevalonii.
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=32044;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90078086; PubMed=2687235;
RA Anderson D.H., Rodwell V.W.;
RT "Nucleotide sequence and expression in Escherichia coli of the 3-
RT hydroxy-3-methylglutaryl coenzyme A lyase gene of Pseudomonas
RT mevalonii."
RL J. Bacteriol. 171:6468-6472 (1989).
DR EMBL; M31807; AAA25894.1; -.
DR GO; GO:0004420; P:hydroxymethylglutaryl-CoA reductase (NADPH). . .; IEA.
DR GO; GO:0009058; P:biogenesis; IEA.
DR InterPro; IPR002202; HMG-CoA red.
DR InterPro; IPR009029; HMG-CoA sub_bind.
DR Pfam; PF00368; HMG-CoA_red; 1.
FT NON_TER 1
SQ SEQUENCE 44 AA; 4925 MW; 9722E2A58DEB5193 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 44;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
DB 14 DEVD 17

RESULT 3
O49798 ID O49798 PRELIMINARY; PRT; 45 AA.
AC O49798;
DT 01-JUN-1998 (T-EMBLrel. 06, Created)
DT 01-JUN-1998 (T-EMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE R2R3-MYB transcription factor (Fragment).
GN ATMYB75.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eustoids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Romero I., Fuentes A., Benito M.J., Malpica J., Leyva A., Paz-Ares J.;
RT "One hundred R2R3-MYB genes in the genome of Arabidopsis thaliana."
RT Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z95798; CAB09230.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001005; MYB_DNA_binding.
DR Pfam; PF00249; myb_DNA-binding; 1.
DR PROSITE; PS50090; MYB_3; 1.
FT NON_TER 1
FT NON_TER 45
SQ SEQUENCE 45 AA; 5308 MW; A5A9E1509F3D6376 CRC64;

Query Match 100.0%; Score 21; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
DB 14 DEVD 17

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Db 19 DEVD 22

RESULT 4
Q97087 ID Q97087 PRELIMINARY; PRT; 45 AA.
AC Q97087;
DT 01-OCT-2001 (T-EMBLrel. 18, Created)
DT 01-OCT-2001 (T-EMBLrel. 18, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Hypothetical protein SPI339.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC BAA-334 / TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Ariguoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae."
RT Science 293:498-506 (2001).
RL EMBL; AE007432; AAK75437.1; -.
DR PIR; D95155; D95155.
DR TIGR; SPI339; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 45 AA; 5089 MW; FOA7B635C2683F20 CRC64;

Query Match 100.0%; Score 21; DB 16; Length 45;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
DB 19 DEVD 22

RESULT 5
Q8FVL6 ID Q8FVL6 PRELIMINARY; PRT; 45 AA.
AC Q8FVL6;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DE Hypothetical protein.
GN BRA0821.
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=1330 / Biovar 1;
RX MEDLINE=22247741; PubMed=12271122;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
RA Dougherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Krahl M., Shetty J., Malek J., Van Aken S.E.,
RA Redmiller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;
RT "The Brucella suis genome reveals fundamental similarities between
RT animal and plant pathogens and symbionts."
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153 (2002).
DR EMBL; AE014576; AAN33996.1; -.

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DR TIGR; BRA0821; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 45 AA; 5041 MW; 7F27B6874E77F886 CRC64;

Query Match 100.0%; Score 21; DB 16; Length 45;
Best Local Similarity 100.0%; Pred. No. 7.2e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 1 DEVD 4
Db 3 DEVD 6

RESULT 6
Q96P95 PRELIMINARY; PRT; 49 AA.
AC Q96P95;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Poly(ADP-ribose) polymerase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA Kang H.S., Park Y.J., Jung H.M., Jun D.Y., Huh T.L., Kim Y.H.;
RT "Characterization of TPA-responsive genes in U937 cells using ordered
RT differential display PCR."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF401218; AL02174.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001510; Znf_PolyADPpol.
DR Pfam; PF00645; zf-PARP; 1.
DR ProDom; PD004675; Znf_PolyADPpol; 1.
DR PROSITE; PS00064; PARP_ZN_FINGER_2; 1.
FT NON_TER 1
FT NON_TER 49
FT NON_TER 49
SQ SEQUENCE 49 AA; 5300 MW; 68F91BA7DABDF4A5 CRC64;

Query Match 100.0%; Score 21; DB 4; Length 49;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
Db 34 DEVD 37

RESULT 7
Q9XVP5 PRELIMINARY; PRT; 49 AA.
AC Q9XVP5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE F35C12.1 protein.
DE F35C12.1
GN F35C12.1
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoides;
OC Rhabditidae; Pterodermidae; Caenorhabditis.
OC NCBI_TaxID=6239;
RN [1]
SEQUENCE FROM N.A.
RA Baynes C.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
SEQUENCE FROM N.A.
RP Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for

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RT investigating biology."
RL Science 282:2012-2018(1999).
DR EMBL; Z81075; CAB03046.1; -.
DR PIR; T21746; T21746.
DR WormPep; F35C12.1; CE09913.
SQ SEQUENCE 49 AA; 5597 MW; 778CB60EB83DPEBE CRC64;

Query Match 100.0%; Score 21; DB 5; Length 49;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
Db 33 DEVD 36

RESULT 8
Q63952 PRELIMINARY; PRT; 50 AA.
AC Q63952;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Endoplasmin (Fragment).
GN GRP94.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10118;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=94148528; PubMed=8314313;
RA De Vouge M.W., Yamazaki A., Bennett S.A., Chen J.H., Shwed P.S.,
RA Couture C., Birnboim H.C.;
RT "Immunoselection of GRP94/endoplasmin from a KNRK cell-specific lambda
RT still library using antibodies directed against a putative heparanase
RT amino-terminal peptide."
RL Int. J. Cancer 56:286-294(1994).
DR EMBL; S69315; AA829919.2; -.
FT NON_TER 50
FT NON_TER 50
SQ SEQUENCE 50 AA; 5478 MW; D8866A965A646117 CRC64;

Query Match 100.0%; Score 21; DB 11; Length 50;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
Db 23 DEVD 26

RESULT 9
Q9IAB6 PRELIMINARY; PRT; 53 AA.
AC Q9IAB6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Smx5 (Fragment).
GN Smx5.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; teleostei; Osteiophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
SEQUENCE FROM N.A.
RA Suellmann H., Murray B.W., Klein J.;
RT "Analysis of Ancient Mhc Class III Synteny by Mapping of Orthologous
RT Genes in the Zebrafish."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF210845; AAF70450.1; -.
DR ZFIN; ZDB-GENE-000616-10; smx5.

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DR GO: 0005634; C:nucleus; IEA.
 DR GO: 0005732; C:small nucleolar ribonucleoprotein complex; IEA.
 DR GO: 0008248; P:pre-mRNA splicing factor activity; IEA.
 DR GO: 0006371; P:mRNA splicing; IEA.
 DR InterPro: IPR006649; snRNP.
 DR InterPro: IPR001163; snRNP_Sm.
 DR Pfam: PF01423; LSM; 1.
 DR ProDom: PD020287; snRNP; 1.
 FT NON TER 1 1
 FT TER 53 53
 SQ SEQUENCE 53 AA; 6078 MW; E70502074A527393 CRC64;

Query Match 100.0%; Score 21; DB 13; Length 53;
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
 Db 48 DEVD 51

RESULT 10

Q98IM8 PRELIMINARY; PRT; 53 AA.
 AC Q98IM8; 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein mar2334.
 GN MSR2334.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Ideawara K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsunoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti.";
 RL DNA Res. 7:331-338(2000).
 DR EMBL: AP002995; BAB49488.1; -;
 KW Hypothetical protein; Complete proteome
 SQ SEQUENCE 53 AA; 5289 MW; B7C5B786C6D8279 CRC64;

Query Match 100.0%; Score 21; DB 16; Length 53;
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
 Db 10 DEVD 13

RESULT 11

Q38258 PRELIMINARY; PRT; 54 AA.
 AC Q38258;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Unidentified ORF15.
 OS Lactococcus phage b1167.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
 OC C2-like viruses.
 OX NCBI_TaxID=36343;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=95111629; PubMed=7812447;
 RA Schouler C., Ehrlich S.D., Chopin M.C.;
 RT "Sequence and organization of the lactococcal prolate-headed b1167
 RT phage genome.";
 RL Microbiology 140:3061-3069(1994).
 DR EMBL: L33769; AAA74352.1; -;
 SQ SEQUENCE 54 AA; 6378 MW; F2D42F16S9BF751 CRC64;

Query Match 100.0%; Score 21; DB 9; Length 54;
 Best Local Similarity 100.0%; Pred. No. 8.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
 Db 10 DEVD 13

RESULT 12

Q38280 PRELIMINARY; PRT; 54 AA.
 AC Q38280; 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE E17 protein.
 GN E17.
 OS Lactococcus bacteriophage C2.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
 OC C2-like viruses.
 OX NCBI_TaxID=31537;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94036453; PubMed=8221377;
 RA Ward L.J., Beresford T.P., Lubbers M.W., Jarvis B.D., Jarvis A.W.;
 RT "Sequence analysis of the lysin gene region of the prolate lactococcal
 RT bacteriophage C2.";
 RL Can. J. Microbiol. 39:767-774(1993).
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=95115663; PubMed=7816023;
 RA Lubbers M.W., Ward L.J., Beresford T.P., Jarvis B.D., Jarvis A.W.;
 RT "Sequencing and analysis of the cos region of the lactococcal
 RT bacteriophage C2.";
 RL Mol. Gen. Genet. 245:160-166(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96086019; PubMed=8534101;
 RA Lubbers M.W., Waterfield N.R., Beresford T.P., Le Page R.W.,
 RA Jarvis A.W.;
 RT "Sequencing and analysis of the prolate-headed lactococcal
 RT bacteriophage C2 genome and identification of the structural genes.";
 RL Appl. Environ. Microbiol. 61:4348-4356(1995).
 DR EMBL: L48605; AAA92163.1; -;
 SQ SEQUENCE 54 AA; 6453 MW; EA5811217531F751 CRC64;

Query Match 100.0%; Score 21; DB 9; Length 54;
 Best Local Similarity 100.0%; Pred. No. 8.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
 Db 10 DEVD 13

RESULT 13

Q84NR3 PRELIMINARY; PRT; 54 AA.
 ID Q84NR3;
 AC Q84NR3;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE P0034A04.6 protein.
 GN P0034A04.6.

OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, PAC
RT clone: P0034A04";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP004333; BAC75552.1; -;
SQ SEQUENCE 54 AA; 6002 MW; 1B425F6484151E8B CRC64;

Query Match 100.0%; Score 21; DB 10; Length 54;
Best Local Similarity 100.0%; Pred. NO. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
DB 35 DEVD 38

RESULT 14
Q977A0
ID Q977A0 PRELIMINARY; PRT; 54 AA.
AC Q977A0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative alcohol dehydrogenase.
GN STS015.
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=111955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JCM 10545 / 7;
RX MEDLINE=21456156; PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankaï A., Koeugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Tanaka J., Kishida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermoacidophilic
RT Crenarchaeon, Sulfolobus tokodaii strain 7.";
RL DNA Res. 8:123-140(2001).
DR EMBL: AF000981; BAB4994.1; -;
DR GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR002085; Adh zn family.
DR Pfam; PF00107; ADH zinc N; I.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 54 AA; 6138 MW; 132B3C067738F740 CRC64;

Query Match 100.0%; Score 21; DB 17; Length 54;
Best Local Similarity 100.0%; Pred. NO. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
DB 16 DEVD 19

RESULT 15
Q99H60
ID Q99H60 PRELIMINARY; PRT; 56 AA.
AC Q99H60;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE RNA-dependent RNA polymerase (Fragment).
OS Human picobirnavirus
OC Viruses; dsRNA viruses; Picobirnavirus.
OX NCBI_TaxID=145856;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=202-FL-97;
RX MEDLINE=20534978; PubMed=11080479;
RA Rosen B.I., Fang Z.Y., Glass R.I., Monroe S.S.;
RT "Cloning of human picobirnavirus genomic segments and development of
RT an RT-PCR detection assay";
RL Virology 277:316-329(2000).
DR EMBL: AF246935; AAG53579.1; -;
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
KW RNA-directed RNA polymerase.
FT NON TER 1 1
FT NON TER 56 56
SQ SEQUENCE 56 AA; 6708 MW; 781490BF8EB423A9 CRC64;

Query Match 100.0%; Score 21; DB 12; Length 56;
Best Local Similarity 100.0%; Pred. NO. 9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
DB 31 DEVD 34

Search completed: May 24, 2004, 14:41:01
Job time : 37.5 secs